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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BREAST AND BT 474 CELLS

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human BT 474 cells is described. Also described are single exon nucleic acid probes expressed in the BT 474 cells and their use in methods for detecting gene expression.

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(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene
expression in a sample derived from human BT 474 cells is described. Also described are single exon nucleic acid probes expressed
in the BT 474 cells and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BREAST AND BT 474
CELLS

5 CROSS REFERENCE TO RELATED APPLICATIONS

The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
10 benefit under 35 U.S.C. s 119(e) of U.S. provisional patent
application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
15 UK patent application no. 0024263.6, filed October 4, 2000,
the disclosures of which are incorporated herein by
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
20 REFERENCE THEREOF

The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
25 triplicate, containing a file named pto_BT474.txt, created
24 January 2001, having 11,325,593 bytes. The Sequence
Listing contained in said file on said disc is incorporated
herein by reference in its entirety.

30 Field of the Invention

The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
35 particular, the present invention relates to unique genome-

derived single exon nucleic acid probes expressed in human BT 474 cells and single exon nucleic acid microarrays that include such probes.

5 Background of the Invention

For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4
10 (1973), these techniques were used principally as tools to further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had
15 been both informed and directed by that antecedent biological understanding.

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane
20 association, and by the predicted assembly of its gene via T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

25 More recently, however, the development of high throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes
30 understanding of the basic biology of the encoded protein product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of
35 mRNA - are of greatest initial interest. This "expressed

sequence tag" ("EST") approach has already yielded vast amounts of sequence data (see for example Adams et al., *Science* 252:1651 (1991); Williamson, *Drug Discov. Today* 4:115 (1999)). For nucleic acids sequenced by this approach, often the only biological information that is known a priori with any certainty is the likelihood of biologic expression itself. By virtue of the species and tissue from which the mRNA had originally been obtained, most such sequences are also annotated with the identity of the species and at least one tissue in which expression appears likely.

More recently, the pace of genomic sequencing has accelerated dramatically. When genomic DNA serves as the initial substrate for sequencing efforts, expression cannot be presumed; often the only a priori biological information about the sequence includes the species and chromosome (and perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence accumulation by directed, EST, and genomic sequencing approaches - and in particular, with the accumulation of sequence information from multiple genera, from multiple species within genera, and from multiple individuals within a species - there is an increasing need for methods that rapidly and effectively permit the functions of nucleic sequences to be elucidated. And as such functional information accumulates, there is a further need for methods of storing such functional information in meaningful and useful relationship to the sequence itself; that is, there is an increasing need for means and apparatus for annotating raw sequence data with known or predicted functional information.

Although the increase in the pace of genomic sequencing is due in large part to technological changes in sequencing strategies and instrumentation, Service, *Science* 280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),

there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears
5 the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found
10 by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST
15 sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of
20 the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and
25 most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function
30 difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al.,
35 *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et

al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,
Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol.*
Biol. 268:78-94 (1997), predict many putative genes without
known homology or function. Such programs are known,
5 however, to give high false positive rates. Burset et al.,
Genomics 34:353-367 (1996). Using a consensus obtained by
a plurality of such programs is known to increase the
reliability of calling exons from genomic sequence.
Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

10 Identification of functional genes from genomic
data remains, however, an imperfect art. For example, in
reporting the full sequence of human chromosome 21, the
Chromosome 21 Mapping and Sequencing Consortium reports
that prior bioinformatic estimates of human gene number may
15 need to be revised substantially downwards. *Nature*
405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus
that permit the functions of the regions identified
bioinformatically – and specifically, that permit the
20 expression of regions predicted to encode protein – readily
to be confirmed experimentally.

Recently, the development of nucleic acid
microarrays has made possible the automated and highly
parallel measurement of gene expression. Reviewed in
25 Schena (ed.), DNA Microarrays : A Practical Approach
(Practical Approach Series), Oxford University Press (1999)
(ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60
(1999); Schena (ed.), Microarray Biochip: Tools and
Technology, Eaton Publishing Company/BioTechniques Books
30 Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from
cDNA/EST libraries, either from those previously described
in the literature, such as those from the I.M.A.G.E.
consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or
35 from the construction of "problem specific" libraries

targeted at a particular biological question, R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes
5 for genes discovered solely by genomic sequencing.

The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of
10 yeast nuclear genes, approximately 95% however, are single exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally
15 been used to probe gene expression from more complex eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the breast are a significant cause of human morbidity and mortality. Increasingly, genetic
20 factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have been identified as causative for some diseases of the breast, for the most part these disorders are believed to have
25 polygenic etiologies. There is a need for methods and apparatus that permit prediction, diagnosis and prognosis of diseases of the human breast, particularly those diseases with polygenic etiology.

30 Summary of the Invention

The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional
35 information derived from genomic sequence. The present

invention also provides apparatus for verifying the expression of putative genes identified within genomic sequence.

In particular, the invention provides novel
5 genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids
10 identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single
15 exon nucleic acid probes for measuring gene expression in a sample derived from human breast, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 5,205 or a complementary sequence, or a portion of such a sequence.

20 By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably
25 amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality
30 of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000
35 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 10,317 or a complimentary sequence, or a
5 portion of such a sequence.

Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp,
10 preferably at least 400bp and, most preferably, 500 bp.

In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least
15 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is
20 preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

25 Preferably, a spatially-addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane
30 which may, preferably, be nitrocellulose or nylon. The nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene,
35 polyacrylate, polymethylmethacrylate, polyvinylchloride,

polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of SEQ ID Nos. 5,206 - 10,317, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 5,205.

Accordingly, in a third aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human breast which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 5,205 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human breast.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOS.: 5,206

- 10,317 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human breast
5 which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOS.: 10,318 - 15,438 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human breast.

10 Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15,
15 suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth
20 aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

25 Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or
30 fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3
35 and Cy5 although other suitable dyes will be known to those

skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer; wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In a sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human Breast, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human Breast; and then measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe, wherein said detectably labeled nucleic acids are derived from mRNA from the Breast of said eukaryote, said

probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

10 identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

20 In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 10,317 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 5,206 - 10,317, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 -5,205.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ ID NOS.: 10,318 - 15,438.

35 Accordingly in a eleventh aspect of the invention

there is provided a peptide comprising a sequence as set out in any of SEQ ID NOS: 10,318 - 15,438, or fragment thereof.

In another aspect, the invention provides means
5 for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated
10 sequence.

Detailed Description of the Invention

15 Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately
20 detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach
25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the
30 term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner
35 et al., Proc. Natl. Acad. Sci. USA 97(4):166501670 (2000);

in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid
5 microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution
10 phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the
15 sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and
20 the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop
25 codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the
30 consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

As used herein, the term "peptide" refers to a
35

sequence of amino acids. The sequences referred to as
PEPTIDE SEQ ID NOS.: are the predicted peptide sequences
that would be translated from one of the exons, or a
portion thereof set out in exon SEQ ID NOS.: The codons
5 encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined
nucleotide sequence or sequences can be and, preferably,
are fragments unique to that sequence or to one or a
combination of those sequences. A fragment unique to a
10 nucleic acid molecule is one that is a signature for the
larger nucleic acid molecule.

As used herein, the phrase "expression of a
probe" and its linguistic variants means that the ORF
present within the probe, or its complement, is present
15 within a target mRNA.

As used herein, "stringent conditions" refers to
parameters well known to those skilled in the art. When a
nucleic acid molecule is said to be hybridisable to another
of a given sequence under "stringent conditions", it is
20 meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding
pair" intends a pair of molecules that bind to one another
with high specificity. Binding pairs are said to exhibit
specific binding when they exhibit avidity of at least 10^7 ,
25 preferably at least 10^8 , more preferably at least 10^9
liters/mole. Nonlimiting examples of specific binding
pairs are: antibody and antigen; biotin and avidin; and
biotin and streptavidin.

As used herein with respect to the visual display
30 of annotated genomic sequence, the term "rectangle" means
any geometric shape that has at least a first and a second
border, wherein the first and second borders each are
capable of mapping uniquely to a point of another visual
object of the display.

35 As used herein, a "Mondrian" means a visual

display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

5

Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and
10 examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in
15 meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

20 FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length
25 shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color
30 hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

35 FIG. 7 is a pictorial representation of the

expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured
5 tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

10 FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a
15 BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases
20 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

25 Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad
30 outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original
35 sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI). Databases of genomic sequence from species other than

human, such as mouse, rat, Arabidopsis, *C. elegans*, *C. brigssii*, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

5 Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to,
10 encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing
15 somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

 The particular genomic sequence to be input into process 200 will depend upon the function for which
20 relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

25 Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic
30 assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

35 The subset of sequences output from process 300

is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

5 Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by
10 incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for
15 incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process
20 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output
25 from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational
30 substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process.
35 Often, data will be stored after each, or at least a

plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence,

either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic,
5 temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts
10 that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST
15 and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

20 If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the
25 database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to
30 report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional
35 preprocessing 24, suitable and specific for the desired

analytical approach and the particular analytical methods thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as
5 processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis.
10 Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

15 Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using
20 programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified
25 algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can
30 be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the
35 undesired sequence as, for example, by converting the

specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after

transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase
5 reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

10 Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to
15 process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report
20 consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7%
25 of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

30 Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process
35 can be repeated on the same input sequence, or subset

thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based inter alia upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully

to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene

calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is
5 conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic)
10 sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500
15 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more
20 effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400
25 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs
30 predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at
35 amplifying pieces of such ORFs is low, and that such

putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been

obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology
5 : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory
10 Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material
15 flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the
20 absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial
25 advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support
30 substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

35 Typically, the support substrate will be glass,

although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, 5 polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even 10 spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

The amplified nucleic acids can be attached 15 covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

20 Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources 25 (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

As is well known in the art, microarrays 30 typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or 35 32 *E. coli* genes suffice to provide a robust measure of

background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural
5 nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the
10 immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates,
15 the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

20 For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using
25 nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid
30 probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For
35 example, each standard microscope slide can include at

least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

5 Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as
10 is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

 The genome-derived single exon microarrays
15 described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3)
20 those constructed from yeast genomic DNA.

 Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above,
25 it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question,
30 R.S. Thomas et al., Cancer Res. (in press). Such microarrays are herein collectively denominated "EST microarrays".

 Such EST microarrays by definition can measure expression only of those genes found in EST libraries,
35 shown herein to represent only a fraction of expressed

genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message
5 successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression
10 measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences
15 that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription,
20 optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor
25 cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from
30 genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST
35 approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

5 As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a
10 spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

 In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention
15 lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T,
20 where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

 A further distinction, which also affects the specificity of hybridization, is occasioned by the typical
25 derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the
30 probes are amplified, rather than excised, from the vector.

 In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from
35 genomic DNA. Typically, therefore, at least about 50, 60,

70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage.

5 Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including
10 probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

15 As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes
20 disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific
25 primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the
30 genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even
35 smaller amount of nonspecific sequence that would

contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the

probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or
5 include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure
10 tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in
15 EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons
20 for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention typically, but need not necessarily, include intronic
25 and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn
30 from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and thus measure such phenomena such as nuclear export control.

35 The genome-derived single exon microarrays of the

present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

5 Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization
10 results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (i.e., mismatched) sequence.

 In contrast, the longer probe length of the
15 genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or
20 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

25 A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound
30 noncovalently to the substrate.

 Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large
35 percentage differences in the theoretically optimum

stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the
5 range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the
10 quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present
15 substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4
20 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons
25 on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm
30 expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50%
35 of protein-encoding genes have introns. In preferred

embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about
5 one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present
10 invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments,
15 through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA
20 sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single
25 cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased
30 commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of nucleotides labeled with a first label, typically a
35 fluorophore (fluorochrome; fluor; fluorescent dye); the

reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes
5 prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned
10 using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

15 Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for
20 subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for further use.

25 Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

30 In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher
35 density arrays, such as are provided by microtiter plates

having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-
5 noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each
10 probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second,
15 different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be
20 packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a
25 genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the
30 genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation
35 information, such as gene expression data. Such recordable

media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then
5 separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should
10 be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and
15 characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic
20 sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected
25 of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences,
30 SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query -
35 including information on identical sequences and

information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence - can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, 5 process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such 10 annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or 15 by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

20 The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the 25 information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively 30 described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an 35 annotated sequence, representation of individual

nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention
5 herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian
10 visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of
15 rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically — for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 — or through user intervention,
20 as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession
25 number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is
30 anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual
35 display 80 is used as a graphical user interface to

computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

5 Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 10 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

 Where a single bioinformatic method or approach 15 identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of 20 horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

 Thus, rectangles 83a in FIG. 3 represent the 25 functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or 30 approach.

 Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from 35 GRAIL or GRAIL II, rectangles 83b can represent the results

from GENEFINDER, and rectangles 83c can represent the results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions. However, the increased visual complexity occasioned by such

display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of

bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as

can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute

expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present

invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of
5 single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present
10 invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example
15 readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 5,205 of these ORFs in BT 474 cells.

20 The BT474 cell line is a human mammary ductal carcinoma cell line that is tumorigenic in nude mice. It was isolated from a solid, invasive ductal carcinoma of the breast, Lasfargues et al., J. Natl Cancer Inst. 61(4):967-78 (1978), and is epithelial and neoplastic. The cell line
25 grows as adherent patches of epithelial cells with compact, multilayered colonies, rarely become confluent.

The cell line is aneuploid human female (XO usually), with most chromosome counts in the hypertetraploid range. Several chromosomes (N11, N13, and N22) are absent, and
30 others are clearly under-represented (N9, N14, and N15) with respect to the other normal chromosomes. Chromosome N7 tends towards over-representation in several karyotypes. Some of the missing normal chromosomes are represented by their involvement in the nine stable marker chromosomes.

35 As would immediately be appreciated by one of skill in

the art, each single exon probe having demonstrable expression in BT 474 cells is currently available for use in measuring the level of its ORF's expression in breast cells.

5 Diseases of the breast are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have been
10 identified as causative for some diseases of the breast, for the most part these disorders are believed to have polygenic etiologies.

For example, according to the American Cancer Society (ACS), carcinoma of the breast is the second most
15 common cancer in women and, after lung cancer, is the second deadliest. The ACS estimates that in the U.S. there occurred 182,800 new cases of malignant breast cancer in 2000, and about 40,800 deaths from the disease. Although incidence of breast cancer is said to have declined, the
20 disease clearly continues to represent a serious risk to the health and life of American women. Indeed, about one in nine U.S. women will develop breast cancer in her lifetime, and at present mortality rates, about a third of such women will eventually die from the disease.

25 A variety of factors are known to increase the risk of breast carcinoma. Sex is one: breast cancer in men is rare. Age is another: as women age, their risk for developing breast cancer increases, a 70 year old woman having three times the risk of developing cancer and five
30 times the risk of dying from the disease as compared to a 40 year old woman. Most breast cancers occur after age 50, although in women with a genetic susceptibility, breast cancer tends to occur at an earlier age than in sporadic cases. Reproductive and menstrual history are also known
35 to affect risk, with risk increasing with early menarche

and late menopause, and is reduced by early first full term pregnancy. Additional risk factors, oft-times termed "lifestyle factors", include weight gain, obesity, fat intake, alcohol consumption, and level of physical
5 activity.

That genetic factors underlie the etiology of breast cancer is suggested by the approximately two-fold increased risk for development of breast cancer by women with a first-degree relative who has also developed breast
10 cancer. After gender and age, a positive family history is the strongest known predictive risk factor for breast cancer. Genetic linkage analysis in families with high rates of inherited cancer have facilitated the identification of several genes in which mutations can be
15 shown to contribute substantially to the development and progression of breast cancer, including BRCA1, BRCA2, p53, and PTEN/MMAC1. Further study has made clear, however, that these genes are not alone sufficient to explain all genetic contributions to breast cancer.

20 For example, BRCA1 appears to be responsible for disease in up to 90% of families with both breast and ovarian cancer, but in only 45% of families with multiple cases of breast cancer without occurrence of ovarian cancer. And mutations in BRCA2, localized to the long arm
25 of chromosome 13, are thought to account for only approximately 35% of multiple case breast cancer families. Furthermore, despite the strong correlation between germline mutations in BRCA1 or BRCA2 and development of breast cancer, only weak connections have been made between
30 these genes and sporadic breast cancer.

Epistatic effects of BRCA1 and BRCA2 mutations on other genetic loci, only some of which have been identified, have been postulated to account for some of the deleterious effects of mutations in these two genes.

35 Thus, mutations in p53 seem to be much more

frequent in BRCA1 breast cancers (20/26) and somewhat more frequent in BRCA2-associated breast cancers (10/22) than in grade-matched sporadic cancers (7/20). BRCA mutation-associated cancers contain p53 mutations not typically
5 found in sporadic breast cancer, and 12 individual hereditary breast cancers have been shown to contain more than a single p53 mutation. Mutations of BRCA1 and BRCA2 may thus confer a "mutator" phenotype permitting the accumulation of genetic abnormalities, with p53
10 inactivation selected during tumor progression.

Additionally, genome-wide screening for chromosomal gains or losses in breast cancers harboring BRCA1 or BRCA2 mutations demonstrated more regions that were amplified or deleted compared to controls, suggesting
15 a generalized increase in large-scale genomic instability. Chromosomes 5q, 4q, and 4p had very frequent loss of heterozygosity in BRCA1 tumors, while BRCA2 tumors were characterized by losses at 13q (near the BRCA2 locus itself) and 6q, and chromosomal gains at 17q (outside of
20 the HER2/neu locus) and 20q.

Mutations of other genes have also been implicated in susceptibility to development or aggressiveness of breast cancer. For example, germline mutations in the ATM gene, localized to chromosome
25 11q22-23, result in an increased risk of breast cancer among female heterozygote carriers with an estimated relative risk of 3.9 to 6.4; it is unclear, however, if mutations in the ATM gene itself contribute to breast cancer.

30 Normal allelic variation in a variety of genes, as opposed to frank mutation, may also influence susceptibility to developing breast carcinoma and the propensity for the disease to progress. Such polymorphisms may thus explain why particular women or
35 ethnic groups who do not otherwise bear mutations in genes

known to be linked to breast cancer are at greater risk, especially in the context of exposure to environmental agents and other nonhereditary risk factors.

Polymorphically expressed genes may code for enzymes that
5 metabolize estrogens or detoxify drugs and environmental carcinogens.

For example, molecular epidemiologic studies of cancer of the breast have examined associations with p450 cytochrome genotypes including CYP1A1, CYP2D6, and CYP17.
10 The CYP1A1 gene, located on chromosome 15q, encodes the enzyme aryl hydrocarbon hydroxylase (AHH), present in breast tissue, and which catabolizes polycyclic aromatic hydrocarbons and arylamines. AHH is strongly inducible, i.e., greater enzymatic activity is seen with greater
15 exposure to substrates. AHH catalyzes the monooxygenation of polycyclic aromatic hydrocarbons to phenolic products and epoxides that may be carcinogenic. AHH is also involved in the conversion of estrogen to hydroxylated conjugated estrogens such as 2-hydroxyestradiol.

20 Three polymorphisms in the CYP1A1 gene have been identified: an MspI RFLP of the 3' end of the gene (MspI); an adenine to guanine mutation in exon 7, causing an isoleucine to valine substitution (Ile-Val); and a polymorphism of the CYP1A1 gene identified among Negroids.
25 The frequencies of the MspI and Ile-Val polymorphisms vary considerably by race, being higher among Japanese and Hawaiian populations as compared with Caucasians and Negroids.

The CYP2D6 gene is located on chromosome 22q and
30 encodes the enzyme debrisoquine hydroxylase, which metabolizes a variety of drugs and other xenobiotics. Like other polymorphically expressed p450 enzymes, it may activate procarcinogens or, conversely, detoxify carcinogens. A number of alleles have been characterized
35 at the CYP2D6 locus. The "poor metabolizer" phenotype

(CYP2D6 mutant/mutant genotype), which is rare in Asians, occurs in about 5% to 10% of Caucasians and in 2% of Negroids.

As another example, the N-acetyl transferase-1 (NAT1) and N-acetyl transferase-2 (NAT2) genes are located on chromosome 8q. Allelic variation in the NAT genes may contribute to variation in populations as to the susceptibility of individuals to development of breast carcinoma, particularly in the context of exposure to compounds present in tobacco. NAT2 detoxifies or, conversely, activates aromatic amines found in tobacco smoke such as 4-aminobiphenyl. Both phenotypic assays and genotypic assays for NAT2 can be used to classify individuals as rapid or slow acetylators. Genetic variants of the NAT2 gene have been cloned and 6 alleles at this locus have been identified: the F1 allele confers the fast acetylator phenotype. The distribution of NAT1 and NAT2 alleles differs widely between racial and ethnic groups.

As yet another example, the glutathione S-transferase-M1 (GSTM1) gene is located on chromosome 1 and the gene for glutathione S-transferase-T1 (GSTT1) is located on chromosome 11q. A glutathione S-transferase-P1 (GSTP1) gene has also been identified. Glutathione S-transferases detoxify a variety of carcinogens and cytotoxic drugs (for example, benzo(a)pyrene, monohalomethanes such as methyl chloride, ethylene oxide, pesticides, and solvents used in industry) by catalyzing the conjugation of a glutathione moiety to the substrate. Allelic variation in the glutathione-S-transferase genes may contribute to variation in populations as to the susceptibility of individuals to development of breast carcinoma, particularly in the context of exposure to environmental toxins. Individuals homozygous for deletions in the GSTM1, GSTT1, or GSTP1 genes may have a higher risk of cancer of the breast and

other sites because of their impaired ability to metabolize and eliminate carcinogens.

GSTM1 is polymorphically expressed and 3 alleles at the GSTM1 locus have been identified: GSTM1-0 (homozygous deletion genotype), GSTM1a, and GSTM1b. The null allele (GSTM1-0) is present in about 38% to 67% of Caucasians and 22% to 35% of Negroids. GSTM is not expressed in breast tissue at high levels. Two functionally different genotypes at the GSTT1 locus have been described: GSTT1-0 (homozygous deletion genotype) and GSTT1-1 (genotypes with 1 or 2 undeleted alleles). A polymorphism of the GSTP1 gene, A313G (changing codon 105 from Ile to Val), has been identified. The GSTT1-0 allele has been associated with accelerated age of first breast cancer diagnosis as compared with the GSTT1-1 allele.

Many other genes have been suggested to be involved in the development and/or progression of breast cancer, either as a result of gain of function or loss of function mutations, or as a result of normal allelic variation within different populations. A nonexhaustive list of such genes, each followed by the gene's chromosomal location, if known, follows: AMPH 7p14-p13; AMPHL (BIN1, SH3P9) 2q14; API4 (survivin, SVV) 17q25(?); ARHA (ARH12, RhoA) 3p21.3; ARHC (RhoC) 1p21-p13; ATM (ATA, ATC) 11q22.3; BAG1 9p12; BARD1 2q34-q35; BCAR1 16q23.1; BCAR2; BCAR3 (NSP2); BCAS1 (NABC1, AIBC1) 20q13.2-q13.3; BRCA1 17q21; BRCA2 13q12.3; CCND1 (D11S287E, Cyclin D, PRAD1) 11q13; CD44 (MDU3, HA, MDU2) 11pter-p13; CD9 (p24, MIC3, BA2) 12p13; CDKN1B (KIP1, P27) 12p13; CDKN2A (P16, INK4A, MTS1) 9p21; COMT 22q11.2; COT (MAP3K8, TPL-2, EST) 10p11.2; CSK (c-src) 15q23-q25; CTSD (CPSD) 11p15.5; CYP17 10q24.3; CYP19 15q21.1; CYP1A1 (CYP1) 15q22-q24; CYP1B1 (GLC3A) 2p22-p21; EFNB2 (EPLG5, LERK5, ephrin-B2) 13q33; EIF3S6 (INT6) 8q22-q23; EIF4E (EIF-4E) 4q21-q25; EMS1 11q13; ERBB2 (HER2, NEU) 17q11.2-q12; ERBB3 (HER3) 12q13; ESR1 (ESRA)

6q25.1; ESR2 (ESRB, ERBeta) 14q; FGF8 (AIGF)
 10q24; GSTM1 (GST1, MU) 1p13.3; GSTP1 (FAEES3, GST3, PI)
 11q13; GSTT1 22q11.23; HRAS 11p15.5; HSPB1 (HSP27) 7q;
 HSPCA (HSP90A , HSPC1); HSPCB (HSP90B, HSPC2) 6p12; IGF1
 5 12q22-q24.1; IGF1R (JTK13) 15q25-q26; IGF2 11p15.5; IL6
 (IFNB2) 7p21; ING1 13q34; KISS1 (KiSS-1) 1q32; KLK3 (PSA,
 APS) 19q13; LASP1 (MLN50) 17q11-q21.3; LIBC 6q22; MAP2K4
 (MKK4, SEK1, JNKK1) 17p11.2; MKI67 (Ki-67) 10q25-qter;
 MMP11 (STMY3, STR3) 22q11.2; MMP2 (CLG4A, CLG4, GELA)
 10 16q13; MUC1 (PUM, PEM) 1q21; MYC (CMYC, C-MYC) 8q24.12-
 q24.13; NOTCH4 (INT3, NOTCH3) 6p21.3; PCNA 20p12; PI5
 (maspin) 18q21.3; PLAUI (uPA , URK) 10q24; PSEN2 (D21S21,
 HPS2, BCEI) 21q22.3; RARB (NR1B2, HAP) 3p24; RB1 (Rb)
 13q14.2; S100A4 (MTS1, P9KA, metastasin) 1q21; SLC22A1L
 15 (BWSCR1A, ORCTL2, IMPT1) 11p15.5; SNCG (BCSG1) 10q23.2-
 q23.3; SRD5A2 2p23; STIP1 (HSP70) 11?; STK11 (LKB1, PJS)
 19p13.3; TFAP2A (AP2 , AP2TF) 6p24; TFAP2B (AP2B) 6p12;
 TFAP2C 20q13.2; TFF1 (D21S21, BCEI) 21q22.3; TGFBR2 3p22;
 TIMP2 17q25; TP53 (p53 , P53) 17q13.1; TPD52 (D52) 8q21;
 20 TPD52L1 (D53, hD53) 6q22-q23; TSG101 11p15.2-p15.1.

The etiology of non-cancerous disorders of the breast may also involve genetic factors. Such disorders include disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast
 25 disease, and non-carcinoma tumors.

Disorders of development of the breast include supernumerary nipples or breasts; accessory axillary breast tissue; congenital inversion of the nipples; and macromastia.

30 Inflammatory diseases of the breast include acute mastitis; periductal mastitis, also called recurrent subareolar abscess and squamous metaplasia of the lactiferous ducts; mammary duct ectasia; fat necrosis; and granulomatous mastitis, including granulomatous lobular
 35 mastitis. Systemic granulomatous diseases that can affect

the breast include Wegener granulomatosis and sarcoidosis.

Proliferative breast diseases include epithelial hyperplasia; sclerosing adenosis; and small duct papillomas. Non-carcinoma tumors include stomal tumors including fibroadenoma and phyllodes tumor, and sarcomas that include angiosarcoma, rhabdomyosarcoma, liposarcoma, leiomyosarcoma, chondrosarcoma and osteosarcoma. Other breast tumors include epithelial cell tumors including large duct papillomas.

10 The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human breast, particularly those diseases with polygenic etiology. With each of the single
15 exon probes described herein shown to be expressed at detectable levels in human breast cancer cells, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

20 For example, diagnosis, grading, and/or staging of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known to be characteristic of a given breast disease, or to specific grades or stages
25 thereof.

 In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the patient's breast to the genome-derived single exon
30 microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids from individuals with known disease. Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed

in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of breast disease to be assessed through the massively parallel determination of altered copy number, deletion, or mutation in the patient's genome of exons known to be expressed in human breast. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art — see Ausubel et al. and Maniatis et al. — each probe reports the level of expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the BT 474 cells has been demonstrated are useful for both measurement in the breast and for survey of expression in other tissues.

Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was

measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence databases.

5 Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

10 The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and for surveying gene expression in the human.

15 Gene expression analysis using microarrays — conventionally using microarrays having probes derived from expressed message — is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

20 Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999);
35 Voehringer et al., "Gene Microarray Identification of Redox

and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

Microarrays have also been used to determine
5 abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al.,
10 "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and
15 Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the
20 Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

25 In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change,
30 serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway
35 of which the gene's expressed protein is a part.

Analogously, where gene expression analysis is used to assess side effects of pharmacological agents - whether in lead compound discovery or in subsequent screening of lead compound derivatives - the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in BT 474 cells.

The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates,

morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a
5 form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known
10 amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO '97/19193 and WO 00/15779. As is well understood, where the probes are
15 to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form
20 suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

25 Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific
30 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3'
35 primers to amplify any one of the probes. The probe

composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 5,206 - 10,317, respectively, for probe SEQ ID NOS. 1 - 5,205. The minimum amount of ORF required to be included in the probe of the present invention in order to

provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 5,206 - 10,317 individually by routine experimentation using standard high stringency
5 conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl
10 poly(dA), 0.2 µg/µl human c_{ot}1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high
15 stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in
20 temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of
25 other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

30 Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are
35 maximally about 5 kb will be used, more typically no more

than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for

ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for
5 hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

10 When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is
15 obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second,
20 different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen
25 for the common attribute of expression in the human BT 474 cells.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell
30 type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF
35 by (i) screening of cDNA libraries; (ii) rapid

amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to
5 provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-
10 derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human BT 474 cells. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group
15 consisting of SEQ ID NOS.: 1 - 5,205.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of
20 probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the
25 same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with
30 a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to
35 their utility as probes of gene expression, particularly as

probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 5,205 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 5,206 - 10,317, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 5,205 can be used, or that portion thereof in SEQ ID NOS. 5,206 - 10,317 used, to express a protein domain by standard in vitro recombinant techniques. See Ausubel et al. and Maniatis et al.

10 Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X[™] Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL[™]) System, New England Biolabs, Beverley, MA)

20 Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, inter alia, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

30 It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 5,206 - 10,317. Such amino acid sequences are set out in SEQ ID NOS: 10,318 - 15,438. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, 35 can be conjugated to a carrier protein and used to generate

antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

5

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

10 Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

Bioinformatics Results

All human BAC sequences in fewer than 10 pieces
15 that had been accessioned in a five month period immediately preceding this study were downloaded from GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the
20 program CROSS_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden
25 Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

30 The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of
35 genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed.

5 That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two
10 criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb
15 window.

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification,
20 as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-
25 modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per
30 gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique
35 5' primer, and a second, different, additional sequence was

commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences
5 also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the
10 universal primers to validate the identity of the amplicon to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto,
15 CA) as template. Each PCR product was verified by SYBR® green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band
20 appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF
25 length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of
30 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about
35 500 bp, it was found that long exons had a higher PCR

failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp,
5 constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and
10 reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear,
15 but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with
20 hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression
25 ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which
30 were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average
35 hybridization signal of which was used as a measure of

background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

5 One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than 1 e^{-100}) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA
10 (BLAST E values from 1 e^{-5} to 1 e^{-99}). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were
15 then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., Nature Genet. 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

20

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase

36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

5

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

10

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) 15 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in 20 each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia 25 Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After

snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5.

10 Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 µl hybridization solution containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c_ot1 DNA, and 0.5 % SDS.

15

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

20

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

25

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter,

30

35

"expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when
5 signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is
10 presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all
15 tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue
20 or cell type. Of the gene elements showing significant signal — where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) — 39% (991) were expressed in all 10 tissues. The next most common class
25 (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

30 FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative
35 expression of a clone in that tissue is indicated at the

respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data – that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

35 Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic

sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays – to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed

high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

10 Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain.				
Microarray Sequence Name	Normalized Signal	Expression Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a

				synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein

				Phosphatase PP2A, neuronal/ downregulates activated protein kinases
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Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be
5 important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
10 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
15 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed
20 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless
25 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to
30 tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2

were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often
 5 used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et
 10 al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1 α (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai et al., *Genomics*
 15 49(2):283-89 (1998)) (AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

20 As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in
 25 choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a
 30 commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH
--

	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 ± 0.11	-1.85 ± 0.08
Brain	-1.41 ± 0.11	-1.17 ± 0.05
BT474	1.85 ± 0.09	1.66 ± 0.12
Fetal Liver	-1.62 ± 0.07	-1.41 ± 0.05
HBL100	1.32 ± 0.05	2.64 ± 0.12
Heart	1.16 ± 0.09	1.56 ± 0.10
HeLa	1.11 ± 0.06	1.30 ± 0.15
Liver	-1.62 ± 0.22	-2.07 ±
Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the

information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb,

upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):

5 red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and
10 12 did not sequence verify.

EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring
15 Human Gene Expression

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique
20 exons in the human genome that could be shown to be expressed at significant levels in BT 474 cells.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon
25 microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the
30 single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 5,205 single exon probes, each fragment corresponding to an extension product from one of
35 the two amplification primers.)

The structures of the 5,205 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 5,205. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 5,206 - 10,317, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered

to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean +
5 (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any
10 signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human BT 474 cells and thus
15 presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human BT 474 cells.

The sequence of each of the exon probes identified by SEQ ID NOS.: 5,206 - 10,317 was individually
20 used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were
25 scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted
30 in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective
35 probes (by "AMPLICON SEQ ID NO.:" and additionally by the

SEQ ID NO:. of the exon contained within the probe:"EXON
SEQ ID NO.:" from least similar to sequences known to be
expressed (i.e., highest BLAST E value), at the beginning
of the table, to most similar to sequences known to be
5 expressed (i.e., lowest BLAST E value), at the bottom of
the table.

Table 4 further provides, for each listed probe,
the accession number of the database sequence that yielded
the "Most Similar (top) Hit BLAST E Value", along with the
10 name of the database in which the database sequence is
found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.
corresponding to the predicted amino acid sequences where
they have been determined for the probe and exon nucleotide
15 sequences. These are set out as PEPTIDE SEQ ID NOS.:. The
peptide sequences for a given exon are predicted as
follows: Since each chip exon is a consensus sequence drawn
from predictions from various exon finding programs (i.e.
Grail, GeneFinder and GenScan), the multiple initial ORFs
20 are first determined in a uniform way according to each
prediction. In particular, the reading frame for predicting
the first amino acid in the peptide sequence always starts
with the first base of any codon and ends with the last
base of non-termination codon. Next, for each strand of the
25 exon, initial ORFs are merged into one or more final ORFs
in an exhaustive process based on the following criteria:
1) the merging ORFs must be overlapping, and 2) the merging
ORFs must be in the same frame.

The Sequence Listing, which is a superset of all
30 of the data presented in Table 4, further includes, for
each probe, the most similar hit, with accession number and
BLAST E value, from the each of the three queried
databases.

Table 4 further lists, for each probe, a portion
35 of the descriptor for the top hit ("Top Hit Descriptor") as

provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as the boundary when only two classes were to be defined for analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ - which is probative evidence that the query sequence has previously been shown to be expressed - the top hit is highly unlikely exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 5,205) and probe exon (SEQ ID NOs.: 5,206 - 10,317, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST

E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

5 (d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

10 EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring Expression of Genes in Human BT 474 cells

Table 4 (214 pages) presents expression, homology, and
15 functional information for the genome-derived single exon probes that are expressed significantly in human BT 474 cells, human epithelial cells isolated from a solid, invasive ductal carcinoma of the breast and available commercially from American Type Culture Collection under
20 catalogue number HTB-20.

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
449	5617	10762	4.28				
890	6040	11211	7.04				
1047	6188		2.6				
1306	6436	11611	12.4				
1627	6765	11949	2.17				
1647	6775	11967	4.24				
1738	6866	12069	1.89				
1761	6887	12083	1.25				
1787	6893	12100	6.38				
1898	7017	12238	0.86				
1880	7097	12328	1.31				
2147	7261	12608	1.73				
2256	7366	12622	2.11				
3167	8316	13480	2.71				
3431	8573	13733	1.47				
3500	8641	13807	11.21				
3547	8688		0.74				
3634	8773	13928	0.83				
3919	9055		0.82				
4169	9295	14433	1.84				
4235	9360	14492	6.08				
4255	9380	14512	0.87				
4255	9380	14513	0.87				
4314	9436		1.18				
4803	9916	15057	1.18				
5026	10128	15257	5.94				
5037	10139	15271	1.46				
2827	7726	12979	2.67	8.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2827	7726	12980	2.67	8.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2889	8043	13207	2.89	8.4E+00	AB043785.1	NT	Mus musculus AT3 gene for antithrombin, complete cds
439	6808	10752	2.06	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
2947	8101	13265	2.66	7.2E+00	L12051.1	NT	Lycopodium obscurum Mill. GTPase (SAR2) mRNA, complete cds

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Table 4
Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2847	8101	13268	2.66	7.2E+00	L12051.1	NT	Lysopeptidase esculentum Mill. GTPase (SAR2) mRNA, complete cds
3510	8651		0.9	6.8E+00	7681657	NT	Homo sapiens DESC1 protein (DESC1), mRNA
4762	9885	15014	1.25	5.3E+00	L43128.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
4036	9167		10.68	4.8E+00	AF186258.1	NT	Emmeline australis histone H3 (H3) gene, partial cds
287	5476	10617	2.31	4.7E+00	BF240552.1	EST_HUMAN	601876854F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4088716 5'
288	5476	10617	1.99	4.7E+00	BF240552.1	EST_HUMAN	601876854F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4088716 5'
3257	8407	13668	1.94	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3012	8168	13323	0.63	4.4E+00	BF630893.1	EST_HUMAN	602072585F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'
3012	8168	13324	0.63	4.4E+00	BF630893.1	EST_HUMAN	602072585F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'
3486	8627	13784	5.32	3.8E+00	X04518.1	NT	N. tabacum chitinase gene 50 for class I chitinase C
4298	8420		0.69	3.8E+00	AF055486.1	NT	Mus musculus seminal vesicle secretory protein 89 (MSVSP89) gene, promoter region
2595	7688		1.75	3.8E+00	AE001582.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
3904	9128	14272	12.69	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
591	5763	10880	9.75	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'
3230	8350	13540	1.12	3.5E+00	AF221538.1	NT	Cryptosporidium falls heat shock protein 70 (HSP70) gene, partial cds
1528	6653	11639	3.27	3.4E+00	AF254577.1	NT	Brassica napus RPB5d mRNA, complete cds
600	6687	10802	1.43	3.2E+00	X98422.1	NT	D. rerio zp-50 POU gene
3999	5687	10802	0.61	3.2E+00	X98422.1	NT	D. rerio zp-50 POU gene
4698	9812	14960	1.65	3.2E+00	4502404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (GEACAM1), mRNA
2788	7856	13121	1.47	3.0E+00	8923884	NT	Homo sapiens hypothetical protein PR000899 (PRO0899), mRNA
2008	7128	12362	1.47	2.9E+00	AE002226.2	NT	Chlamydia pneumoniae AR39, section 83 of 94 of the complete genome
1469	6588	11784	7.24	2.8E+00	AF188398.1	NT	Bufo marinus maturation K (matK) gene, partial cds; chloroplast gene for chloroplast product
1643	6771		1.94	2.8E+00	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
228	5423	10560	13.15	2.7E+00	6878308	NT	Mus musculus per-hexamer repeat gene 3 (Phor3), mRNA
228	5423	10561	13.15	2.7E+00	6878308	NT	Mus musculus per-hexamer repeat gene 3 (Phor3), mRNA
4646	9764	14908	5.56	2.6E+00	AF068749.1	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
1476	6803	11788	1.77	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
1476	6803	11789	1.77	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
2894	8138	13303	0.95	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
4881	8992	15139	5.5	2.4E+00	4503352	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
1257	6386	11563	11.36	2.3E+00	Z46724.1	NT	G. adamsii artificial single chain antibody gene (L3)
4063	9222		1.44	2.3E+00	AJ401081.1	NT	Bos taurus partial cyto gene for cytochrome b
3992	9128	14271	1.39	2.2E+00	AF020528.1	NT	Magnaporthe oryzae Class IV chitin synthase (chs4) gene, complete cds

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Table 4
Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4280	9412	14847	3.83	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4280	9412	14548	3.83	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
568	7884	10881	6.54	2.1E+00	AF132612.2	NT	Mus musculus pre-7 cell receptor alpha gene, enhancer region and upstream region
3576	8716		0.76	2.1E+00	AW449388.1	EST_HUMAN	UHRB13-ak-e-08-QJ(a1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
1189	6332	11501	1.31	2.0E+00	AF180527.1	NT	Homo sapiens p22Dkdel (DOKDEL) mRNA, complete cds
1189	6332	11502	1.31	2.0E+00	AF180527.1	NT	Homo sapiens p22Dkdel (DOKDEL) mRNA, complete cds
1340	6468	11649	0.86	2.0E+00	AF204827.1	NT	Oryctolagus cuniculus Nbr-K+ATPase beta 1 subunit mRNA, complete cds
1588	6717		2.41	2.0E+00	P25593	SWISSPROT	PUTATIVE RNA METHYLTRANSFERASE SPB1
2133	7247	12492	10.19	2.0E+00	Z78279.1	NT	R. norvegicus mRNA for collagen alpha1 type I
2133	7247	12493	10.19	2.0E+00	Z78279.1	NT	R. norvegicus mRNA for collagen alpha1 type I
4076	8206	14342	1.8	2.0E+00	AW684498.1	EST_HUMAN	h113c06.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
4076	8206	14343	1.9	2.0E+00	AW684498.1	EST_HUMAN	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
3086	8218	13371	1.87	1.8E+00	P21004	SWISSPROT	h113c05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
3087	8250	13398	1.92	1.8E+00	U04356.1	NT	PROTEIN B8 PRECURSOR
3087	8250	13400	1.92	1.8E+00	U04356.1	NT	Synethococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
1108	8247	11410	2.85	1.7E+00	Q60114	SWISSPROT	Synethococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
2250	7360	12617	1.65	1.7E+00	AL163280.2	NT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE)(SUCROSE 6-FRUCTOSYL TRANSFERASE)
2363	7460	12716	0.88	1.7E+00	AI141097.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
4438	9557	14699	0.76	1.7E+00	Q60114	SWISSPROT	oz43h05.x1 Soares_NHIMP_L1 Homo sapiens cDNA clone IMAGE:1678137 3'
2028	7145	12385	4.48	1.6E+00	AF189339.1	NT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE)(SUCROSE 6-FRUCTOSYL TRANSFERASE)
2037	7155	12394	2.2	1.6E+00	AF077974.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2041	7168	12398	1.19	1.6E+00	Y11344.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2260	7370		1.16	1.6E+00	X98373.1	NT	Mus musculus ST6GalNAcII gene, exon 2
2630	8084	13251	1.56	1.6E+00	W58426.1	EST_HUMAN	B. napus gene encoding endo-polygalacturonase
4006	9138		5.78	1.6E+00	BF670077.1	EST_HUMAN	z026101.r1 Soares_fetal_heart_NH-H19W Homo sapiens cDNA clone IMAGE:341689 5' similar to gb:D229805 N-ACETYLACTOSAMINE SYNTHASE (HUMAN);
4329	8451	14594	1.52	1.6E+00	AF159327.1	NT	602186095T1 NIH_MCC_45 Homo sapiens cDNA clone IMAGE:4310691 3'
4329	8451	14586	1.52	1.6E+00	AF159327.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds

Table 4

Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5087	10168	15303	2.59	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
6087	10169	16304	2.63	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
31	5242	10358	3.73	1.6E+00	U63448.1	NT	Rattus norvegicus Jun dimerization protein 2 (Jdp-2) mRNA, complete cds
230	5424	10502	2.47	1.6E+00	AE002201.2	NT	Chlamydia pneumoniae AR39, section 32 of 94 of the complete genome
618	5778		2.04	1.5E+00	8752981	NT	Mus musculus a disintegrin and metalloprotease domain (ADAM) 15 (metagdn) (Adam15), mRNA
2387	7493	12746	1.38	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2486	7690	12839	1.38	1.5E+00	8678360	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3116	7493	12746	2.41	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3366	8401	13889	0.8	1.5E+00	AE001945.1	NT	Deinococcus radiodurans R1 section 82 of 228 of the complete chromosome 1
28	5239	10354	1.12	1.4E+00	7691695	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
28	5239	10355	1.12	1.4E+00	7691695	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
2319	7423		5.46	1.4E+00	U67022.1	NT	Ovis aries prion protein gene, complete cds
2830	7728	12884	1.41	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2735	7828	13083	227.51	1.4E+00	AF084584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2735	7828	13084	227.51	1.4E+00	AF084584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3316	8482		0.8	1.4E+00	5453733	NT	Homo sapiens Mad4 homolog (MAD4) mRNA
4569	8677		1.87	1.4E+00	BF681547.1	EST_HUMAN	602156687/F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4287555 5'
5031	10133	15263	0.92	1.4E+00	Y18213.1	NT	Homo sapiens putative psfHbA pseudogene for hair keratin, exons 2 to 7
669	5733		1.6	1.3E+00	Z73640.1	NT	Munodo gene encoding 4-Dihydroxyethyl-lisopropyl dehydrogenase
903	6053	11223	2.66	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 25S rRNA gene, isolate Tibet
1130	6287		29.68	1.3E+00	Y18213.1	NT	Homo sapiens putative psfHbA pseudogene for hair keratin, exons 2 to 7
1301	6431	11605	12.87	1.3E+00	4507898	NT	Homo sapiens zinc finger protein 167 (ZNF167) mRNA
1301	6431	11606	12.87	1.3E+00	4507898	NT	Homo sapiens zinc finger protein 167 (ZNF167) mRNA
1363	6482		1.49	1.3E+00	U61730.2	NT	CotA leucine-3-oxo acid dehydrogenase (cotA) gene, complete cds
1623	6751		2.09	1.3E+00	AE002339.2	NT	Chlamydia muridarum, section 68 of 85 of the complete genome
2521	7625		1.26	1.3E+00	BE068735.2	EST_HUMAN	801661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3'
2806	8058	13227	0.74	1.3E+00	6756621	NT	Mus musculus alpha-spectrin 1, erythrocyte (Sptn1), mRNA
3583	8724	13882	0.82	1.3E+00	AF016484.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P85), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-protease enhancer protein (PCOLCE) genes, complete c-
649	5810	10945	8.47	1.2E+00	AA676246.1	EST_HUMAN	212208.01 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431535 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
824	5977	11141	1.11	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-II)
824	5977	11142	1.11	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-II)
824	5977	11143	1.11	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-II)
870	6020		1.11	1.2E+00	8924234	NT	Human sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1163	6288	11464	6.19	1.2E+00	AF080245.2	NT	Eliaia olivaria sesquiterpene synthase mRNA, complete cds
1208	6340	11510	1.88	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1208	6340	11511	1.88	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2366	7483	12718	0.88	1.2E+00	AF158465.1	NT	Human sapiens post-synaptic density 85 (DLG4) gene, complete cds
3036	8238	13388	0.95	1.2E+00	AB020881.1	NT	Human sapiens mRNA for KIAA0874 protein, partial cds
3144	8265	13483	5.63	1.2E+00	AL181583.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3144	8265	13484	5.63	1.2E+00	AL181583.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3270	8419		3.42	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3336	8482	13649	0.85	1.2E+00	AF188740.1	NT	Human sapiens LHX3 gene, intron 2
3691	8829	13983	7.07	1.2E+00	U75802.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 8, partial cds
3961	9056	14248	1.8	1.2E+00	BF373570.1	EST_HUMAN	MR0-FT0175-050900-203-g08_1 FT0175 Homo sapiens cDNA
4274	8482	13948	1.07	1.2E+00	AF188740.1	NT	Human sapiens LHX3 gene, intron 2
4450	9588		1.82	1.2E+00	M87060.1	NT	Rattus rattus cardiac AE3 gene, exons 1-23
4497	8916	14757	1.04	1.2E+00	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4534	9852	14797	1.81	1.2E+00	AF158465.1	NT	Human sapiens post-synaptic density 85 (DLG4) gene, complete cds
4682	9880		5.91	1.2E+00	Y09200.1	NT	T. pirnatum chloroplast rbcL gene, partial
463	5631	10770	1.04	1.1E+00	D86880.1	NT	Human mRNA for KIAA0227 gene, partial cds
1773	6899	12107	1.22	1.1E+00	AV199393.1	EST_HUMAN	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
3311	8458	13820	6.79	1.1E+00	AL163213.2	NT	Human sapiens chromosome 21 segment HS21C013
3311	8458	13821	6.79	1.1E+00	AL163213.2	NT	Human sapiens chromosome 21 segment HS21C013
3486	8810	13776	0.7	1.1E+00	8922841	NT	Human sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3567	8708	13888	0.62	1.1E+00	AI083600.1	EST_HUMAN	wf64h11.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to
3688	8836	13989	1.48	1.1E+00	AE003886.1	NT	SW-PE81_HUMAN Q12888 P83-BINDING PROTEIN 53BP1 ;
3688	8836	13990	1.49	1.1E+00	AE003886.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3705	8832		0.73	1.1E+00	X65374.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3916	9051	14210	1.01	1.1E+00	8922841	NT	H. parahaemolyticus hphIM(A), hphIM(C), hphIR and menB genes
3995	9126	14273	0.79	1.1E+00	8755205	NT	Human sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
4189	9315		6.62	1.1E+00	9836331	NT	Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Pamb7), mRNA
4655	9772		1.78	1.1E+00	U34992.1	NT	R. uncinus complete mitochondrial genome
							Carcharias plumbeus 19 lambda light chain gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4978	10088	15221	3.5	1.1E+00	U18468.1	NT	African swine fever virus, complete genome
85	6304		2.28	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
109	6313	10452	1.86	1.0E+00	D88428.1	NT	Canis cubensis mRNA for cerine/threonine kinase, complete cds
417	5685		2.14	1.0E+00	AB021884.1	NT	Marchantia polymorpha genes for 26S rRNA, 6S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
574	5738	10835	2.43	1.0E+00	AL251680.1	NT	Grandidia lignina mRNA for homeodomain transcription factor (so gene)
678	5834	10974	8.37	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
677	5835		1.3	1.0E+00	AF125984.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1395	7918		2.27	1.0E+00	X60416.1	NT	V. carteri Agal-CAM mRNA
2459	7563	12815	1.02	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2459	7563	12816	1.02	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2841	7998	13154	3.76	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1)(SR TYPE 1)
2841	7998	13155	3.76	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1)(SR TYPE 1)
2838	8090		0.76	1.0E+00	O14226	SWISSPROT	HYPOTHETICAL 67.8 KD PROTEIN CBP12.08G IN CHROMOSOME 1
3182	8333	13498	1.13	1.0E+00	AA628453.1	EST_HUMAN	af28408.s1 Soares_tetal_fetus_NL2HFB_9v Homo sapiens cDNA clone IMAGE:1032830 3' similar to
3685	6304		0.73	1.0E+00	U23808.1	NT	WP:C42D8.3 CE04204; contains element MER22 MER22 repetitive element
3659	8797	13953	1.44	1.0E+00	AJ223816.1	NT	Xenopus laevis rhodopsin gene, complete cds
						NT	Agaricus bisporus mRNA for tyrosinase
4044	8179	14316	0.8	1.0E+00	AF223391.1	NT	Homo sapiens cation channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4249	9374		0.68	1.0E+00	B822245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
4773	9898	15032	3.01	1.0E+00	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
8134	10234		0.63	1.0E+00	AF200817.1	NT	Pilot whale morbillivirus phosphoprotein (P) gene, partial cds
3590	8730		8.61	9.8E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
521	6687	10819	1.66	9.8E-01	P22697	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYL-GLUTAMATE SYNTHASE)(AGS)(NAGS)
2782	7856		1.19	9.8E-01	AF174644.1	NT	Xenopus laevis rpo GTPase mRNA, complete cds
4418	9536	14674	0.66	9.8E-01	AF197925.1	NT	Brassica inermis putative cytosolic phosphoglucuronase (pgm1) mRNA, complete cds
4418	9536	14675	0.66	9.8E-01	AF197925.1	NT	Brassica inermis putative cytosolic phosphoglucuronase (pgm1) mRNA, complete cds
4437	9556	14698	1.62	9.8E-01	AF178874.1	EST_HUMAN	PM2-UM0053-240800-005-F12 UM0053 Homo sapiens cDNA
3781	8898	14048	1.82	9.5E-01	BE902340.1	EST_HUMAN	801875639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3761	8898	14049	1.92	9.5E-01	BE902340.1	EST_HUMAN	801875639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3184	8336		3.87	9.4E-01	AF165990.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (polB) gene, partial cds
3203	8364		1.88	9.4E-01	AF080585.1	NT	Pimpla brachycarpa zinc finger protein (ZFP1) mRNA, complete cds

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Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1745	6871		1.14	9.3E-01	AF242382.1	NT	Homo sapiens phytenyl-CoA hydroxylase (PHYH) gene, exon 6
2599	7699	12954	2.9	9.3E-01	BE071172.1	EST_HUMAN	RC5-BT0503-271189-011-801 BT0503 Homo sapiens cDNA
4009	9142	14282	0.78	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4009	9142	14283	0.78	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
3224	8374	13537	3.14	9.2E-01	BE022702.1	EST_HUMAN	601441393T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3'
2116	7231		1.21	9.1E-01	8923056	NT	Homo sapiens hypodermal protein FLJ20048 (FLJ20048), mRNA
3189	8340	13501	1.03	9.1E-01	T26418.1	EST_HUMAN	AB200G8R infant brain, LLNL array of Dr. M. Soares 1N1B Homo sapiens cDNA clone LLAB200G8 5'
3189	8340	13502	1.03	9.1E-01	T26418.1	EST_HUMAN	AB200G8R infant brain, LLNL array of Dr. M. Soares 1N1B Homo sapiens cDNA clone LLAB200G8 5'
3181	8342	13506	0.76	9.0E-01	7661625	NT	Homo sapiens DKKFZP684M2423 protein (DKKFZP684M2423), mRNA
4358	9480	14618	1.77	9.0E-01	AF093810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
5001	10106	16237	0.6	9.0E-01	AF017726.1	NT	Oryzalogus cuticularis Rad51 (RAD51) mRNA, complete cds
4516	8633	14778	1.69	8.8E-01	O26350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
484	6632	10771	1.49	8.7E-01	AF108953.2	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2360	7488	12740	1.03	8.7E-01	5901893	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
2839	7894	13162	13.39	8.7E-01	AA636863.1	EST_HUMAN	nt05911.at NCI_CGAP_P4.1 Homo sapiens cDNA clone IMAGE:1076877
4894	10100		3.43	8.7E-01	AF121970.1	NT	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put-
474	5941		2.14	8.6E-01	X17012.1	NT	Rat GFII gene for insulin-like growth factor II
839	6010	11182	6.02	8.6E-01	W69089.1	EST_HUMAN	z044e03.1 Soares_fetal heart NBH18W Homo sapiens cDNA clone IMAGE:343518 5'
3602	8741	13896	0.86	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 83
3778	8915	14067	1.3	8.6E-01	U49724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds
740	8898	11048	2.34	8.3E-01	M89437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3088	8221	13372	3.2	8.3E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3887	9121	14268	2.82	8.3E-01	Y16177.1	NT	Streptomyces antibioticus polyketide biosynthesis gene cluster
2044	7160	12399	1.35	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
3440	8582	13742	2.55	8.1E-01	AF055068.1	NT	Homo sapiens MHC class I region
3440	8582	13743	2.55	8.1E-01	AF055068.1	NT	Homo sapiens MHC class I region
4901	10012		0.83	8.1E-01	AF202684.1	NT	Drosophila melanogaster Naik-ATPase beta subunit isoform 4 (Ybeta2) mRNA, complete cds
172	5367		2.34	8.0E-01	AJ271610.1	NT	Staphylococcus aureus partial pta gene for phosphate acyltransferase allele 16
288	5475	10616	12.82	8.0E-01	AJ132721.1	NT	Bos taurus tub and rif genes
1613	6741	11936	0.96	8.0E-01	8394037	NT	Rattus norvegicus protease (prosome, macrophage) 28 subunit, alpha (Pum91), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2026	7147		1	8.0E-01	BF630982.1	EST_HUMAN	802072473F1 NCI_QGAP_Bm87 Homo sapiens cDNA clone IMAGE:4215091 5'
3049	8203	13359	1.08	8.0E-01	AF127897.1	NT	Salivari belmensis olfactory receptor (SBO27) gene, partial cds
3294	8441	13603	1.1	8.0E-01	AB006183.1	NT	Mus musculus gene for olfactory G-protein, complete cds
3680	8816		1.68	8.0E-01	AL162768.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 7/7
4507	8828	14769	6.59	8.0E-01	X63739.2	NT	Gallus mRNA for ribosomal acetylcholine receptor (nAChR) beta 3 subunit
4866	10074	15212	1.12	8.0E-01		NT	Mus musculus myosin IXb (My9b), mRNA
483	5621	10764	0.97	7.9E-01	D11476.1	NT	Lymnaea dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
743	6870		0.73	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 69 of the complete genome
1618	6746		10.36	7.9E-01	AB040883.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
1688	6797		0.99	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 64 of 163 of the complete genome
2243	7364	12611	4.46	7.9E-01	AB004816.1	NT	Oryzias latipes curculin mRNA for mitogen-activated protein kinase, complete cds
2244	7355	12612	1.07	7.9E-01	AF130469.1	NT	Danio rerio Tsp4-associated protein Tap1A (tap1A) mRNA, complete cds
3501	8642	13808	2.76	7.9E-01	AF228864.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4277	9400		1.82	7.9E-01	BE263612.1	EST_HUMAN	801192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4683	9701	14839	0.91	7.9E-01	8763746	NT	Mus musculus embigin (Emb), mRNA
4583	9701	14840	0.91	7.9E-01	8763745	NT	Mus musculus embigin (Emb), mRNA
5140	10240		0.65	7.9E-01	AF139718.1	NT	Chrysomya bezziana peritrophin-48 precursor, gene, complete cds
5168	10258	16397	1.26	7.9E-01	AF228843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
877	6027		1.78	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone o-1kh04
2254	7964	12620	1.48	7.8E-01	AW959567.1	EST_HUMAN	EST371637 MAGE resequencer, MAGE Homo sapiens cDNA
4670	9768	14931	1.11	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc9H1 mRNA, complete cds
5019	10121		0.75	7.8E-01	AW763353.1	EST_HUMAN	RC3-CT0254-130100-023-c02 CT0254 Homo sapiens cDNA
136	5336	10480	4.5	7.7E-01	AF184346.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
724	6880						Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Ia) and major histocompatibility protein class II beta chain (Ib) genes, complete cds; butyrophilin-like (N99), butyrophilin-4
2873	7770	13022	1.32	7.7E-01	AF050157.1	SWISSPROT	CITRATE SYNTHASE
3337	8483		0.76	7.7E-01	8893408	NT	Homo sapiens UDP-N-acetyl-alpha-D-glucosamine:polypeptide N-acetylglucosaminyltransferase 7 (GALNAc-T7) (GALNAc-T7) mRNA
3586	8726	13884	3.69	7.7E-01	AF118085.1	NT	Homo sapiens PRO1875 mRNA, complete cds
4375	9486	14840	3.06	7.7E-01	AF189486.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4376	8498	14841	3.08	7.7E-01	AF189488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
511	5877		1.28	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
592	5745	10873	1.08	7.5E-01	AF20503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 6
3341	8487	13653	0.98	7.9E-01	G14203.1	EST_HUMAN	G14203 Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu
1131	6288	11430	1.4	7.4E-01	AI589148.1	EST_HUMAN	tr14008.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu
2324	7432	12684	0.99	7.4E-01	AB011108.1	NT	repetitive element; contains element MIR repetitive element
3707	8946	13999	1.07	7.4E-01	AF112638.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
3878	8014	14171	0.63	7.4E-01	AF133310.1	NT	Malva pusilla actin (Act1) mRNA, complete cds
4288	8410	14548	7.33	7.4E-01	AL163248.2	NT	Vibrio cholerae phage CTXphi Calcutta-rsR-a (rsR-a) and Calcutta-rsR-b (rsR-b) genes, complete cds
2989	8123	13288	0.83	7.3E-01	P09710	SWISSPROT	Homo sapiens chromosome 21 segment HS21C046
4587	8706	14843	0.76	7.3E-01	AE01108.1	NT	HYPOTHETICAL PROTEIN HKLF1 (IRL1) (TRL1)
4609	8785	14930	4.1	7.3E-01	AF228421.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
832	6984		1.44	7.2E-01	L29281.1	NT	Homo sapiens HT017 mRNA, complete cds
1861	7078	12302	7.26	7.2E-01	X78140.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
3039	8193	13348	1.3	7.2E-01	AF108100.1	NT	N. tabacum NtF-4A13 mRNA
3434	8578	13738	2.23	7.2E-01	AF068808.1	NT	Fowlpox virus, complete genome
4735	8848	14894	3.18	7.2E-01	D80314.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6/A-1 allele, complete cds
5088	10198	15338	1.13	7.2E-01	AF108778.1	NT	Lmesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5098	10188	15337	1.13	7.2E-01	AF108778.1	NT	Homo sapiens transcription factor TCF-4 gene for T-cell transcription factor-4, exons 15-16
690	6847	10990	8.62	7.1E-01	D21070.1	NT	Homo sapiens transcription factor TCF-4 gene for T-cell transcription factor-4, exons 15-16
3036	8189	13345	12.51	7.1E-01	AJ270777.1	NT	isoform (RyR1), complete cds
4180	8308	14442	3.32	7.1E-01	7305380	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4180	8308	14443	3.32	7.1E-01	7305380	NT	Mus musculus obogelin (Obog), mRNA
1232	6963	11636	1.84	7.0E-01	AB014514.1	NT	Mus musculus obogelin (Obog), mRNA
1232	6963	11538	1.84	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1232	6963	11538	1.84	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5038	10140		1.55	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
5168	10288	15407	3.65	7.0E-01	T68328.1	EST_HUMAN	yc41h03.s1 Stratagene liver (#637224) Homo sapiens cDNA clone IMAGE:63285 3' similar to gb:K03020 PHENYLALANINE-4-HYDROXYLASE (HUMAN);
871	6118	11287	13.08	6.8E-01	U69674.1	NT	Candida albicans squelens epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
971	6118	11288	13.08	6.9E-01	U69674.1	NT	Candida albicans squelens epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1314	6444	11621	1.88	6.9E-01	AA593530.1	EST_HUMAN	m28a09.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085178 3'
3204	8355	13516	1.41	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
858	6108	11275	1.78	6.8E-01	AF017784.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2835	7733		2.28	6.8E-01	D80917.1	NT	Synschochysia sp. PCC8803 complete genome, 2727, 3418852-3573470
2789	6756	11950	1.22	6.8E-01	AA854475.1	EST_HUMAN	q75a05.s1 Soares_papillary tumor_NbHPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to gb:X56411_jm1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4544	8882	14605	1.28	6.8E-01	J00782.1	NT	Rat(hooded) prolactin gene : exon iii and flanks
288	5484	10628	24.41	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
337	5520	10656	18.88	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
2131	7245	12489	1.07	6.7E-01	AA451884.1	EST_HUMAN	2x12g12.s1 Soares_total_fetus_Nb2HFB_9w Homo sapiens cDNA clone IMAGE:788310 3' similar to contains element TART repetitive element ;
2148	7634	12509	1.89	6.7E-01	AF185073.1	NT	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
2884	8118	13281	3.1	6.7E-01	8678580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4431	6550	14683	0.64	6.7E-01	X74421.1	NT	S.tuberosum mRNA for glucose-6-phosphate dehydrogenase
4947	10056	15194	1.03	6.7E-01	AW078110.1	EST_HUMAN	xa95g12.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:2874588 3'
2881	7767	13008	1.24	6.6E-01	AF188339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3470	8612	13778	1.02	6.6E-01	4506880	NT	Homo sapiens serpin domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
3635	8774	13930	3.76	6.6E-01	Y07889.1	NT	C.albicans random DNA marker, 282bp
4085	9214		0.72	6.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofel gene, and sodium phosphate transporter (NPT3) gene, complete cds
5170	10288	15408	1.21	6.6E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
622	5782	10912	1.19	6.5E-01	M75140.1	NT	H.vulgaria Na,K-ATPase alpha subunit mRNA, complete cds
822	6782	10913	1.19	6.5E-01	M75140.1	NT	H.vulgaria Na,K-ATPase alpha subunit mRNA, complete cds
3414	8567	13718	4.01	6.5E-01	AB041226.1	NT	Mus musculus gene for Tob2, complete cds
4268	9381	14614	4.73	6.5E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
5045	10147	15278	2.82	6.5E-01	U28921.1	NT	Phaeodactylum subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
249	5440	10580	6.59	6.4E-01	U48948.1	NT	Drosophila melanogaster skd dyadema chain mRNA, complete cds
3438	8680	13740	3.28	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3840	8978	14131	1.22	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1807 protein, partial cds
433	5602	10749	3.11	6.3E-01	P08228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
533	5689	10831	1.69	6.3E-01	U32889.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2144	7258	12504	1.04	6.3E-01	U81138.1	NT	Shigella flexneri multi-antigen resistance locus
2642	7645	12895	35.38	6.3E-01	U76331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2842	7645	12898	35.38	6.3E-01	U76331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2987	8142		0.7	6.3E-01	Y17275.1	NT	Lycopodium obscurum pds gene, complete CDS
2371	7477		2.11	6.1E-01	6878078	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
5182	10289	15428	1.04	6.1E-01	BF314193.1	EST_HUMAN	601801013F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130378 6'
484	5681	10797	1.02	6.0E-01	D87876.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
590	5725		2.77	6.0E-01	6802959	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (GLA20), mRNA
1371	8498	11882	1.83	6.0E-01	AF065253.1	NT	Human respiratory syncytial virus strain CH69-53b attachment protein (G) gene, complete cds
3782	8929	14077	0.82	6.0E-01	AJ233386.1	NT	Viral haemorrhagic septicaemia virus N, P, M, G, N, L genes, French strain 07-71
4007	9140	14281	1.3	6.0E-01	X16842.1	NT	Xenopus mRNA for desmin
4169	9285		1.94	6.0E-01	AF058895.1	NT	Homo sapiens Natch3 (NOTCH3) gene, exons 26, 27, and 28
1001	8147	11314	2.24	6.0E-01	U82701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
1409	6538	11714	1.11	5.9E-01	6680232	NT	Mus musculus 3-hydroxy-3-methylglutaryl-Coenzyme A lyase (Hmgcl), mRNA
3263	8403	13664	5.03	5.9E-01	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
3263	8403	13665	5.03	5.9E-01	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4188	9323		5.04	5.9E-01	AF162766.1	NT	Rattus norvegicus ceradn 2 mRNA, partial cds
1013	7032	12252	1.08	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN
3857	9082	14244	1.09	5.8E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4076131 5'
4488	8907	14745	4.59	5.8E-01	AB030977.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
4765	9878		0.92	5.8E-01	AF110846.1	NT	Megascalia scalaris sex-lethal homolog (Meglsl) gene, partial cds, alternatively spliced products
1507	6834	11820	0.98	5.7E-01	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
1607	6834	11821	0.98	5.7E-01	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3015	8169		0.87	5.7E-01	6755293	NT	Mus musculus placentaloma variant translocation 1 (Pvt1), mRNA
3208	8359	13520	1.87	5.7E-01	Q8WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVOT1) (MOVOT1)
3487	8828		2.48	5.7E-01	AB033903.1	NT	Populus euphratica pease-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
6183	10280	15418	1	5.7E-01	L41887.1	NT	Drosophila extra sex combis gene, exon 1-4, complete cds
3345	8491	13657	1.31	5.8E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3345	8491	13658	1.31	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
4218	8343	14473	1	5.8E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
1214	8346	11516	2.85	5.8E-01	8393912	NT	Rattus norvegicus Prothymosin A carboxylase, beta polypeptide (Pcb), mRNA
2682	7758	13009	2.01	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2682	7758	13010	2.01	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2884	8038	13203	0.84	5.5E-01	5802085	NT	Homo sapiens superkiller viral-like activity 2 (S. coronavirus homolog)-like (SKIV2L), mRNA
3038	8182	13533	1.83	5.6E-01	H48219.1	EST_HUMAN	yo18a10.a1 Soares adult brain N25gHB56Y Homo sapiens cDNA clone IMAGE:178288 3'
3219	8370	13533	3.87	5.6E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3687	8806	13982	2.13	5.5E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
140	6337	10481	12.97	5.4E-01	7657288	NT	Homo sapiens KIAA0929 protein Mix2 interacting nuclear target (MINT) homolog (KIAA0928), mRNA
140	6337	10482	12.97	5.4E-01	7657289	NT	Homo sapiens KIAA0929 protein Mix2 interacting nuclear target (MINT) homolog (KIAA0928), mRNA
583	6748	10874	1.14	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
583	6748	10875	1.14	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
1275	8404	11578	2.32	5.4E-01	AW88087.1	EST_HUMAN	QV4-NN0040-070400-180-604 NN0040 Homo sapiens cDNA
2097	7212	12602	2.04	5.4E-01	AED02247.2	NT	Chlamydia pneumoniae AR39, section 74 of 84 of the complete genome
2235	7347	12602	1.13	5.4E-01	AJ276882.1	NT	Drosophila melanogaster mRNA for 15,16' beta carotene dioxygenase (beta-diox gene)
							Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), component C2 (C2) genes; and complement component C2 (C2) genes
514	5880	10814	2.01	5.3E-01	AF019413.1	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2744	7838	13092	12.78	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2744	7838	13093	12.78	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3227	8377	13538	3.1	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LISCL) gene, complete cds

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Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4184	8310		1.28	5.3E-01	U38687.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
817	5970	11131	9.27	5.2E-01	L20770.1	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1188	6301	11487	6.81	5.2E-01	Q8WV30	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5)
1183	6327	11494	3.63	5.2E-01	AF224492.1	NT	(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1884	7013		4.02	5.2E-01	AL163285.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
2130	7244	12468	1.48	5.2E-01	AB018283.2	NT	Homo sapiens chromosome 21 segment HS21C085
3080	8249	13398	1.39	5.2E-01	U65942.1	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3222	8373		0.68	5.2E-01	D73443.1	NT	Chlamydomonas reinhardtii strain S2833 POM191A and POM190A precursor, genes, complete cds
3386	8630		1.73	5.2E-01	AL110780.1	NT	Asciobacter vinelandii lsd gene for isocitrate dehydrogenase, complete cds
3425	8567	13726	2.15	5.2E-01	AA884165.1	EST_HUMAN	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3612	8751		1.26	5.2E-01	AF020268.1	NT	am77005.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:1618504 3'
4054	8751		0.64	5.2E-01	AF020268.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mch) mRNA, nuclear gene encoding chloroplast protein, complete cds
5114	10215		1.1	5.2E-01	AF020268.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mch) mRNA, nuclear gene encoding chloroplast protein, complete cds
614	5774	10605	2.44	5.1E-01	M58509.1	NT	Homo sapiens chromosome 21 segment HS21C081
647	5808	10942	4.08	5.1E-01	AJ233944.1	NT	Human adrenocortical reductase gene, exons 3 to 12
647	5808	10943	4.08	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
1685	6793		1.04	5.1E-01	X87895.1	NT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
4052	9183	14325	4.76	5.1E-01	A1858495.1	EST_HUMAN	R. norvegicus mRNA for mammalian fusca protein
4168	9284	14420	2.65	5.1E-01	P06390	SWISSPROT	wf39b12.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2427263 3'
3634	8763	13948	1.16	5.0E-01	AE001785.1	NT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
3728	8868	14020	0.77	5.0E-01	U55574.1	NT	Thermoplasma maritima section 87 of 138 of the complete genome
3809	8948	14086	1.12	5.0E-01	L38483.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 383p.138, partial cds
3851	8987	14142	3.05	5.0E-01	AB033010.1	NT	Rattus norvegicus jagged protein mRNA, complete cds
780	6944	11104	1.23	4.9E-01	BF571462.1	EST_HUMAN	Homo sapiens mRNA for KIAA1184 protein, partial cds
1672	6801	11898	2.2	4.9E-01	AJ243958.1	NT	802078649F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1811	7630	12280	1.11	4.9E-01	U40659.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
3526	8688		1.14	4.8E-01	AA912942.1	EST_HUMAN	Canis porcellus pulmonary surfactant protein A (SP-A) mRNA, complete cds
3932	8068		1.38	4.7E-01	BE407975.1	EST_HUMAN	g52a09.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:16287144 3'
3724	8882	14015	1.52	4.6E-01	BF693300.1	EST_HUMAN	601286358F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3628188 5'
3724	8882	14016	1.52	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5117	10218		1.06	4.6E-01	M11267.1	NT	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
							Bovine steroid 21-hydroxylase gene (P-450-c21) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2834	7889	13148	4.74	4.5E-01	AA677088.1	EST_HUMAN	245d02.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3288	8445	13807	4	4.5E-01	Q05783	SWISSPROT	BASEMENT MEMBRANE SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)
3359	8504	13871	1.01	4.5E-01	Q28247	NT	Mus musculus DNA polymerase epsilon catalytic subunit (Pde) gene, exons 2 through 12
4001	9194	14323	1.29	4.5E-01	AF126378.1	SWISSPROT	COLLAGEN ALPHA 5(N) CHAIN
4060	9181	14323	1.02	4.5E-01	AF178908.1	EST_HUMAN	498609.x1 Barstead coria HPLRB8 Homo sapiens cDNA clone IMAGE:2353480 3'
4147	10317	15172	4.15	4.5E-01	AF178908.1	EST_HUMAN	h06002.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
4920	10030	15172	1.18	4.5E-01	BE963448.1	EST_HUMAN	60165725F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3'
2030	7148		2.19	4.4E-01	6880503	NT	Mus musculus Integral membrane-associated protein 1 (Imap1), mRNA
2368	7472	12727	2.49	4.4E-01	P49765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3286	8443	13605	1.3	4.4E-01	AF068780.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3286	8443	13605	1.3	4.4E-01	AF058780.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3300	8447	13609	2.03	4.4E-01	BF058728.1	EST_HUMAN	791d02.y1 NC1_CGAP_B18 Homo sapiens cDNA clone IMAGE:3389795 5'
4213	8358	10726	1.54	4.4E-01	BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606383 5'
410	5578	10726	2.01	4.3E-01	AF155218.1	NT	Caillitrix jacchus MW/LW opsin gene, upstream flanking region
410	5578	10727	2.01	4.3E-01	AF155218.1	NT	Caillitrix jacchus MW/LW opsin gene, upstream flanking region
1617	6745	11840	1	4.3E-01	AW866550.1	EST_HUMAN	QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA
2836	7891	13341	1.95	4.3E-01	AW866550.1	EST_HUMAN	QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA
3032	8186	13341	0.81	4.3E-01	AW866550.1	EST_HUMAN	QV4-SN0024-200400-183-b01 SN0024 Homo sapiens cDNA
4123	9251	14368	1.16	4.3E-01	J00308.1	NT	Human somatostatin I gene and flanks
4385	5578	10726	1.2	4.3E-01	AF155218.1	NT	Caillitrix jacchus MW/LW opsin gene, upstream flanking region
4385	5578	10727	1.2	4.3E-01	AF155218.1	NT	Caillitrix jacchus MW/LW opsin gene, upstream flanking region
4838	10046		1.1	4.3E-01	AL161502.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
6094	10194		0.89	4.3E-01	9835260	NT	Xestia cingulum granubius, complete genome
1367	7915	11678	1.08	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
3593	8732	13886	4.15	4.2E-01	AE003947.1	NT	Xyella fastidiosa, section 83 of 228 of the complete genome
3615	8734	13910	0.97	4.2E-01	AE003947.1	EST_HUMAN	q94601.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878945 3'
9680	10318		0.67	4.2E-01	N81203.1	EST_HUMAN	788E1 fetal brain cDNA Homo sapiens cDNA clone 788E1-K similar to R07879, Z40498
3857	8903	14150	0.82	4.2E-01	AW835527.1	EST_HUMAN	QVQ-LT0018-180200-127-t01 LT0018 Homo sapiens cDNA
3965	9090	14243	1.14	4.2E-01	Q04888	SWISSPROT	SOX-8 PROTEIN
4886	9782	14928	5.49	4.2E-01	AA634083.1	EST_HUMAN	q98401.s1 NC1_CGAP_P10 Homo sapiens cDNA clone IMAGE:597777 similar to gb:IM33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4748	8881	16010	3.83	4.2E-01	R13467.1	EST_HUMAN	y177e01.t1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1085	6233	11398	1.46	4.1E-01	AI805481.1	EST_HUMAN	RC-BT091-210188-142 BT091 Homo sapiens cDNA
1104	6242	11406	1.2	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1104	6242	11406	1.2	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
2672	7768	13020	1.06	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2606	8059	13228	1.98	4.1E-01	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2606	8059	13228	1.98	4.1E-01	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
4248	8379	14506	3.92	4.1E-01	AL124920.1	NT	Rhodospirillum rubrum sp. AD45 isoA, isoB, isoC, isoD, isoE and isoF genes
4282	9405		0.72	4.1E-01	AA608267.1	EST_HUMAN	om3402 s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1642819 3'
4637	9755	14802	1.1	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5'
4632	9769	14916	1.23	4.1E-01	AA480067.1	EST_HUMAN	z06607.1 Soares_total_fetus_Nb2HF8_Sw Homo sapiens cDNA clone IMAGE:788428 5'
1041	6181	11346	0.86	4.0E-01	8404868	NT	Leaues rubellus mitochondrion, complete genome
1344	6473	11653	1	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dm) mRNA, complete cds
1495	6622		2.81	4.0E-01	6878258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
2766	5334	10478	2.2	4.0E-01	6878490	NT	Mus musculus ubiquitin-protein ligase 63 component n-recogin (Ubr1), mRNA
2637	8081	13257	1.3	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2637	8081	13258	1.3	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
							Streptococcus pneumoniae Y1C (MIC), Y1D (VID), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3672	8811	13969	2	4.0E-01	AF088003.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3608	8949	14091	3.15	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3608	8949	14092	3.16	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4788	8989		8.37	4.0E-01	Q31949	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
1387	6815	11697	1.52	3.8E-01	AF208618.1	NT	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds
2605	7704	12860	2.05	3.8E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2667	7763	13013	2.88	3.8E-01	XB2032.1	NT	H. sapiens B-myb gene
2667	7763	13014	2.88	3.8E-01	XB2032.1	NT	H. sapiens B-myb gene
3070	6223	13374	4.04	3.8E-01	AJ226888.1	NT	Shorthorn mellioli egl, eglB2, eglC3 genes and orf3
4056	9186	14328	1.34	3.8E-01	BF692611.1	EST_HUMAN	761d01.X1 NC1 CGAP_B16 Homo sapiens cDNA clone IMAGE:3339169 3'
4677	10085	16220	1.68	3.8E-01	BE726867.1	EST_HUMAN	601.653948F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833689 5'
155	6352		13.75	3.8E-01	7018483	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
605	6671		9.81	3.8E-01	AB029281.1	NT	Mus musculus pom-1 mRNA for pericentriolar material-1, complete cds
2636	7639	12887	3.74	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
2597	7645	12951	2.31	3.8E-01	6878002	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
2673	8127		0.91	3.8E-01	AJ251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 88SE-MP1213)

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3020	8174	13332	1.93	3.8E-01	AF043383.1	NT	Pleuronectes americanus aminopeptidase N (amipN) gene, partial cds
3465	8607	13771	7.75	3.8E-01	AL161618.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3540	8667		0.92	3.8E-01	AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2367856 3'
3737	8975	14028	0.98	3.8E-01	BE154080.1	EST_HUMAN	PMO-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
4040	9171	14312	0.76	3.8E-01	AJ277381.2	NT	Takifugu rubripes wnt2 (partial), frank1, cfr and frank2 (partial) genes
5030	10132	16262	1.07	3.8E-01	AF038683.1	NT	Homo sapiens Mpv17 protein (MPV17) gene, partial cds; and uncortin gene, complete cds
2484	7658	12809	4.15	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3442	8584	13746	8.82	3.7E-01	AF066336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
3849	8885	14141	0.7	3.7E-01	AA319482.1	EST_HUMAN	EST121715 Adrenal gland tumor Homo sapiens cDNA 5' end
4207	9332	14485	6.9	3.7E-01	AJ218707.1	EST_HUMAN	ol39e07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1610188 3'
4297	9419	14552	1.3	3.7E-01	AW878837.1	EST_HUMAN	MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
4368	9489	14633	9.03	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 208 of the complete genome
258	6448	10587	0.84	3.6E-01	AJ008908.1	NT	Brasileia nepus mRNA for MAP4K alpha2 protein
998	6142		8.33	3.6E-01	U89241.1	NT	Human mltp gene, partial cds
1318	6447	11828	2.64	3.6E-01	T80255.1	EST_HUMAN	y039e06.r1 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:24443 5'
1318	6447	11827	2.84	3.6E-01	T80255.1	EST_HUMAN	y039e06.r1 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:24443 5'
1919	7038	12288	3.85	3.6E-01	AW590184.1	EST_HUMAN	hg33i02.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2947419 3'
1919	7038	12269	3.85	3.6E-01	AW590184.1	EST_HUMAN	hg33i02.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2947419 3'
1956	7073	12288	3.28	3.6E-01	AF218207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2387	7473		1.87	3.6E-01	X76725.1	NT	P. Irregularis (P3804) gene for actin
2884	10314		6.6	3.6E-01	AF169486.1	NT	Drosophila melanogaster sugar transporter 3 (suc3) mRNA, complete cds
3481	8593	13759	2.12	3.6E-01	X76738.1	NT	H. sapiens serotonlin transporter gene, exons 9 and 10
3451	8593	13757	2.12	3.6E-01	X76738.1	NT	H. sapiens serotonlin transporter gene, exons 9 and 10
4388	9508	14848	1.13	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA
4688	9802	14948	0.97	3.6E-01	AF071838.1	NT	Mus musculus protein tyrosine kinase Tec (Tec) gene, alternative exons 4 and 4a, exons 5 through 7 and Tec isoform, complete cds
4688	9802	14949	0.97	3.6E-01	AF071838.1	NT	Mus musculus protein tyrosine kinase Tec (Tec) gene, alternative exons 4 and 4a, exons 5 through 7 and Tec isoform, complete cds
4720	9834	14978	0.86	3.6E-01	Y11528.1	NT	Z. mays mRNA for casein kinase II alpha subunit
4761	9874	15028	1.32	3.6E-01	AJ229237.1	NT	Bacteria from anoxic bulk soil 16S rRNA gene (strain XB45)
4897	10103	16234	2.4	3.6E-01	AW339393.1	EST_HUMAN	ha02g04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872668 3'
111	5315	10464	0.83	3.5E-01	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
206	5401	10543	2.38	3.5E-01	6978933	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
723	5879	11027	1.02	3.5E-01	7706193	NT	Homo sapiens GAP-like protein (LOC51308), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
723	6878	11028	1.02	3.5E-01	7706138	NT	Homo sapiens GAP-like protein (LOC51308), mRNA
780	5835	11093	2.69	3.5E-01	BF129786.1	EST_HUMAN	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
1831	6760	11856	1.07	3.5E-01	BF310686.1	EST_HUMAN	801894653F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124244 5'
1851	6778	11971	2.33	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2259	7369	12825	1.03	3.5E-01	P08788	SWISSPROT	HOMEOBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3)
2571	7944	12926	2.4	3.5E-01	AA223252.1	EST_HUMAN	z08a09.at Strabagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'
2686	7762		1.11	3.5E-01	U05897.1	NT	Fibroblast succinoglycerase S85 endoglucanase E (celE) and endoglucanase D (celD) genes, complete cds
3784	8921		1.46	3.5E-01	AA642138.1	EST_HUMAN	nt60d03.s1 NCI CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172357 3'
4236	9391	14493	1.81	3.5E-01	AF071263.1	NT	Danio rerio homeobox protein (hox4b) gene, complete cds
4911	10021	15168	5.47	3.5E-01	M18348.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
705	5882		1.51	3.4E-01	AL242958.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E8, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
877	6123	11293	5.3	3.4E-01	Y09788.2	NT	Pseudomonas fluorescens coR, cds genes, orf222 and partial lnaA gene
1331	6480	11639	2.1	3.4E-01	Y00554.1	NT	Azobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2379	7485	12739	2	3.4E-01	D90909.1	NT	Synochocystis sp. PCC6803 complete genome, 1127, 1311235-1430418
2971	8125	13288	0.68	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2971	8125	13289	0.68	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3127	8279	13435	0.68	3.4E-01	D90909.1	NT	Synochocystis sp. PCC6803 complete genome, 1127, 1311235-1430418
3140	8291	13448	0.65	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3325	8472	13634	0.7	3.4E-01	AF034882.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3518	8659	13826	5.42	3.4E-01	AF106835.1	NT	Methylothermus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3769	8906		2.04	3.4E-01	BF449010.1	EST_HUMAN	7n84d01.x1 NCI CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3872232 3' similar to TR:Q8UJ15
4010	9143		0.92	3.4E-01	AF194614.1	NT	Q8UJ15 DJ18C9.1 ;
4028	9157		1.3	3.4E-01	AA564198.1	EST_HUMAN	Homo sapiens p47-phox (NGF1) gene, complete cds
4813	9731	14868	1.67	3.4E-01	BE08912.1	EST_HUMAN	no11b10.s1 NCI CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4830	10040		4.7	3.4E-01	AL240873.1	EST_HUMAN	MR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
13	5224	10336	7.33	3.3E-01	X07850.1	NT	q195c05.x1 NCI CGAP_K1d3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element
							Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene

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Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
102	5224	10338	3.16	3.3E-01	X07880.1	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
447	5616	10761	1.27	3.3E-01	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
632	5793	10927	1.14	3.3E-01	7662485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1203	6336	11507	5.33	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1311	6441	11618	2.69	3.3E-01	BF568880.1	EST_HUMAN	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
1366	6495	11677	1.22	3.3E-01	U43626.1	NT	Human chromosome 15q11-q13 putative DNA replication origin in the g-aminobutyric acid receptor b3 and e5 gene cluster
1618	6747	11841	1.68	3.3E-01	6753685	NT	Mus musculus disintegrin 5 (Dign5), mRNA
1760	6876		2.18	3.3E-01	AA332794.1	EST_HUMAN	EST136722 Embryo, 8 week 1 Homo sapiens cDNA 6' and
2362	7488		2.55	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (uridine phosphorylase) transferase and orotidine-5'-
2816	8069	13241	2.39	3.3E-01	AJ251805.1	NT	Bacteriophage phi-Y608-12 complete genome
2868	8141		0.83	3.3E-01	Q02743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION
3027	8181	13337	0.77	3.3E-01	AJ007832.2	NT	FACTOR 35 KD SUBUNIT (CLMF P35)
3476	8818	13784	1.16	3.3E-01	AB012822.1	NT	Streptomyces argillaceus methylglucosyl biosynthesis genes
3767	8924	14074	1.88	3.3E-01	Q84645	SWISSPROT	Homo sapiens MTA1-L1 gene, complete cds
3798	8933	14080	1.12	3.3E-01	P22602	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3838	8974	14229	1.96	3.3E-01	AL161498.2	NT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1), HELPER COMPONENT
3978	9110	14258	1.82	3.3E-01	AF200446.1	NT	PROTEINASE (HC-PRO); PROTEIN P3)
4348	9468		3.16	3.3E-01	D31662.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4660	9778		1.49	3.3E-01	A1639114.1	EST_HUMAN	Hypoxanthine phosphoribosyl transferase gene, partial cds
4805	9817	15058	1.12	3.3E-01	D64003.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
486	5624		1.78	3.2E-01	AF018281.1	NT	bp78b12 nt NCL CGAP U19 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gbX37522 ANTIGEN
716	5873		0.62	3.2E-01	AL161561.2	NT	PEPTIDE TRANSPORTER 1 (HUMAN);
1164	6299	11463	11.49	3.2E-01	AF047013.1	NT	Synedocystis sp. POC8803 complete genome, 22/27, 2755705-2888768
1266	6415	11681	1.65	3.2E-01	Z60202.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
1397	6525	11704	5.03	3.2E-01	Q48824	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1764	6910	12118	1.45	3.2E-01	Z60041.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1784	6920	12130	3.16	3.2E-01	AW667194.1	EST_HUMAN	P. vulgaris atcs-1 gene
1784	6920	12131	3.15	3.2E-01	AW667194.1	EST_HUMAN	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
2142	7256	12502	1.18	3.2E-01	BF203817.1	EST_HUMAN	S. cerevisiae chromosome II reading frame ORF YBR172e

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2512	7815		1.28	3.2E-01	7710078	NT	Mus musculus Pibofonated 1 homeobox (Pibofon1), mRNA
3085	8248	13397	0.85	3.2E-01	BF380745.1	EST_HUMAN	IL2-UT0073-180800-161-H11 UT0073 Homo sapiens cDNA
3824	8080		0.85	3.2E-01	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
4316	9438	14571	1.15	3.2E-01	4758185	NT	Homo sapiens synplekin (SYM) mRNA
4372	9493	14637	1.41	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4476	8598	14735	1.26	3.2E-01	Q10288	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4708	9822		7.84	3.2E-01	BF383617.1	EST_HUMAN	80208197ZF1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4248505 5'
4817	9928	15070	1.1	3.2E-01	4587688	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
5188	10285	15421	1.32	3.2E-01	AL161514.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 28
2632	7730	12987	1.38	3.1E-01	R18051.1	EST_HUMAN	yes9108.1 Scores Total liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:126051 5' similar to gbtM64241 OM PROTEIN (HUMAN);
2858	7878	13004	2.82	3.1E-01	7681871	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2858	7878	13005	2.82	3.1E-01	7681871	EST_HUMAN	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2821	7877		1.08	3.1E-01	AW629436.1	EST_HUMAN	h44h08.x1 Scores S1 Homo sapiens cDNA clone IMAGE:2876391 3'
3163	8304		3.28	3.1E-01	AB028089.1	NT	Mus musculus gene for Ser/Thr kinase KUAMRE, exon 8
3884	9020	14177	1.15	3.1E-01	AJ251588.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
4942	10052	15180	0.84	3.1E-01	AE003984.1	NT	Xiella fastidiosa, section 130 of 228 of the complete genome
71	7859	10418	1.35	3.0E-01	8756083	NT	Mus musculus protein kinase C, epsilon (Piso), mRNA
251	6442	10582	7.54	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1226	6358	11528	2.11	3.0E-01	AW300400.1	EST_HUMAN	yes3108.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774349 3'
1623	6850	11838	3	3.0E-01	AJ008755.1	NT	Balanoptera physalus gene encoding atrial natriuretic peptide
2977	8131		1.03	3.0E-01	AB008877.1	NT	Bos taurus mRNA for UDP-glucuronosyltransferase, complete cds
3188	8339		0.98	3.0E-01	X63615.1	NT	S.pombe plc1 gene
3188	8347		1.28	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alyPG gene for polyglutamate lyase, complete cds
3844	8980	14135	1.71	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0282-281189-001-g01 ST0282 Homo sapiens cDNA
3947	9082	14234	0.82	3.0E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4487	9608	14744	1.8	3.0E-01	AJ008755.1	NT	Balanoptera physalus gene encoding atrial natriuretic peptide
2228	7341	12894	1.01	2.9E-01	AF222718.1	NT	Chrysodidymus syndicus mitochondrion, complete genome
3163	8316	13478	1.05	2.9E-01	AF078111.1	NT	Xenopus laevis transcription factor E2F mRNA, complete cds
3234	8884	13546	3.86	2.8E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171289-001-f12 CT0328 Homo sapiens cDNA
3234	8884	13546	3.66	2.8E-01	AW754239.1	EST_HUMAN	PM1-CT0328-171289-001-f12 CT0328 Homo sapiens cDNA
3873	9009	14185	0.83	2.8E-01	AJ810836.1	EST_HUMAN	p21a1.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:016060 NIL-2-A ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4047	9178	14319	0.84	2.8E-01	AB016428.1	NT	Cavia porcellus mRNA for glutathione s-transferase, complete cds
4062	9183		0.85	2.8E-01	AW002802.1	EST_HUMAN	w02f10.x1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:2480395 3'
4484	9588	14721	0.94	2.8E-01	AA284468.1	EST_HUMAN	z557d12.r1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701691 5' similar to contains Alu repetitive element
4657	9774		0.73	2.8E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
5012	10115	19248	5.24	2.8E-01	BF104760.1	EST_HUMAN	601822439F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045618 5'
5012	10115	15247	5.24	2.8E-01	BF104760.1	EST_HUMAN	601822439F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045618 5'
5086	10196		1.02	2.8E-01	AB070898.1	EST_HUMAN	w06803.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2287309 3' similar to contains L1.12 L1 repetitive element
5205	10302	16438	0.81	2.8E-01	AV724733.1	EST_HUMAN	AV724733 HTB Homo sapiens cDNA clone HTBCFC05 5'
587	5782		3.2	2.8E-01	U87136.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP180 mRNA, complete cds
572	5736		1.03	2.8E-01	L28145.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1084	6223	11390	2.84	2.8E-01	AF168050.1	NT	Guinea guinea oocyte maturation factor Moe (c-mos) gene, partial cds
1281	6410	11685	0.65	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163888 5'
1281	6410	11686	0.65	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163888 5'
1285	6424	11597	0.84	2.8E-01	D88950.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1740	6867	12072	2.48	2.8E-01	AW560020.1	EST_HUMAN	QV1-CT0394-12020-055-505 GT0394 Homo sapiens cDNA
2009	7127	12369	1.22	2.8E-01	AL047820.1	EST_HUMAN	DKFZp68882321_j1 588 (synonym: hufb1) Homo sapiens cDNA clone DKFZp68882321
2122	7237	12480	0.98	2.8E-01	AW511195.1	EST_HUMAN	h44403.x1 Soares_NFL_Y_GBC_S1 Homo sapiens cDNA clone IMAGE:2812333 3'
2447	7551	12804	1.43	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1683 section 384 of 400 of the complete genome
2447	7551	12805	1.43	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1683 section 384 of 400 of the complete genome
2518	7622		1.06	2.8E-01	AL161555.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2628	7725	12878	1.18	2.8E-01	AB020976.1	NT	Arabidopsis thaliana mRNA for lipopolysaccharase, complete cds
2640	8094		1.32	2.8E-01	AF178480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
2941	8095	13281	2.3	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
2941	8095	13282	2.3	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
3241	8391	13553	0.73	2.8E-01	4603842	NT	Homo sapiens coagulation factor V (proaccelerin, labile factor) (F5) mRNA
3360	8505	13672	0.88	2.8E-01	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (417)
3971	9105	14253	1.57	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4096	9225		0.62	2.8E-01	AE004450.1	NT	Pseudomonas aeruginosa PAO1, section 11 of 529 of the complete genome
4170	9286		2.1	2.8E-01	AI090888.1	EST_HUMAN	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element; contains element MER22 repetitive element
4434	9553	14698	0.94	2.8E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magea8 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4439	8458	14700	2.82	2.8E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4750	8833	15012	0.98	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB9, complete cds
4750	8833	15013	0.98	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB9, complete cds
4781	8904	16044	0.9	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
4787	8910	15051	2.63	2.8E-01	AF030164.1	NT	Bovine adenovirus 3 complete genome
4830	8942	15084	1.1	2.8E-01	BF528188.1	EST_HUMAN	602042801F1 NCI_CGAP_Bn07 Homo sapiens cDNA clone IMAGE:4180129 5'
4855	8967	15112	2.48	2.8E-01	A1272699.1	EST_HUMAN	qf59c11.x1 Soares_NIHMPU_S1 Homo sapiens cDNA clone IMAGE:1876828 3' similar to contains Alu repetitive element;
476	5843	10784	2.44	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
610	5770	10889	3.75	2.7E-01	AA460081.1	EST_HUMAN	z038b10.s1 Soares_total Jettus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element
1265	6394	11908	2.01	2.7E-01	AB004806.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1653	6782	11908	1.82	2.7E-01	X76815.1	NT	Q Lambias SR2 gene
1742	6868	12073	2.26	2.7E-01	W58087.1	EST_HUMAN	z022h10.j1 Soares_total Jettus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:341443 5'
1788	6912	12120	1.11	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2124	7933		1.08	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular stomatitis transporter type 2, promoter region and exon 1
2347	7454	12707	3.72	2.7E-01	Y13888.1	NT	Feline immunodeficiency virus env gene, isolate ITT0088PIU (M88), partial repetitive element
2432	7636	12789	2.19	2.7E-01	AI310858.1	EST_HUMAN	ta43c11.x2 NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1
2853	8107		0.77	2.7E-01	BF088284.1	EST_HUMAN	CM1-HT0875-06000-385-e05 HT0875 Homo sapiens cDNA
3986	8120	14267	1.84	2.7E-01	AI928015.1	EST_HUMAN	w082e11.x1 NCI_CGAP_KG11 Homo sapiens cDNA clone IMAGE:2482828 3'
3996	8130	14274	0.88	2.7E-01	AF218214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
3996	8130	14275	0.88	2.7E-01	AF218214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4002	8135	14278	2.24	2.7E-01	L77689.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
4865	8977	15123	0.66	2.7E-01	L27516.1	NT	Triticum aestivum (Wc966) gene, complete cds
5023	10126		3.3	2.7E-01	AW866131.1	EST_HUMAN	RC1-CT0288-230200-018-e03 CT0288 Homo sapiens cDNA
488	7891	10777	3.04	2.6E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
480	5848		1.09	2.6E-01	D10469.1	NT	Bos taurus mRNA for mb-1, complete cds
1400	8528	11707	1.48	2.6E-01	BE885087.1	EST_HUMAN	601510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912346 5'
1447	8575	11761	1.26	2.6E-01	AB013290.1	NT	Glycine max pseudogene for B0 30K
1903	7022	12241	4.04	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1903	7022	12242	4.04	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2

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Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2084	7200		4.41	2.6E-01	AW733182.1	EST_HUMAN	bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M86072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14888_cds1 Mouse surfact locus surfact 3 protein gene (MOUSE);
2448	7552		2.33	2.6E-01	Y12858.1	NT	B. maritimus fbcd. gene
2517	7621		4.2	2.6E-01	BE272440.1	EST_HUMAN	801126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:289004S 5'
3069	8219		1.12	2.6E-01	AW874631.1	EST_HUMAN	EST386835 MAGE resequences, MAGM Homo sapiens cDNA
3569	8709	13870	0.82	2.6E-01	M22342.1	NT	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3621	8780	13917	2.13	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLO) gene, exons 1A, 2, 3, 4, and 5
4076	9206	14341	0.69	2.6E-01	AW959510.1	EST_HUMAN	EST371680 MAGE resequences, MAGF Homo sapiens cDNA
4126	9264	14393	15.62	2.6E-01	BE090598.1	EST_HUMAN	QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA
4334	9456	14593	1.09	2.6E-01	AF176283.1	NT	Enterococcus faecium strain N97-330 varD glycopeptide resistance gene cluster, complete cds; and unknown gene
4470	9589	14728	0.87	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4470	9589	14729	0.87	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4621	9639	14786	1.38	2.6E-01	AA457617.1	EST_HUMAN	aa88d07.1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4618	9734	14871	2.81	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*) mRNA, complete cds
4683	9789	14944	1.44	2.6E-01	AF142703.1	NT	Ophiostoma radiosa maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
4858	10064	15203	3.82	2.6E-01	H04893.1	EST_HUMAN	yf51e05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:162288 5'
238	5431	10570	1.47	2.6E-01	4502298	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP6D), nuclear gene encoding mitochondrial protein, mRNA
239	5431	10570	1.65	2.5E-01	4502298	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP6D), nuclear gene encoding mitochondrial protein, mRNA
252	5443		4.63	2.6E-01	M28601.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
833	5985	11162	1.13	2.5E-01	U09984.1	NT	Mus musculus ICR(Swiss) glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1081	6202		0.83	2.5E-01	AE002159.1	NT	Ureaplasma urealyticum section 97 of 59 of the complete genome
1122	6260	11426	10.45	2.5E-01	T88837.1	EST_HUMAN	yv11g07.r1 Stragene lung (8537210) Homo sapiens cDNA clone IMAGE:117468 6'
1388	6516		0.88	2.5E-01	AB026343.1	NT	Olea europaea OEW mRNA for lipoel synthase, complete cds
1741	6888		3.12	2.5E-01	4885406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1891	7929	12230	1.19	2.5E-01	BE68604.1	EST_HUMAN	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
1891	7929	12231	1.19	2.5E-01	BE68604.1	EST_HUMAN	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2384	7480		2.19	2.6E-01	AE000876.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2467	7571		1.12	2.6E-01	AA251987.1	EST_HUMAN	2s11a12.1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:694862 5'
3394	8538		3.28	2.6E-01	AW973471.1	EST_HUMAN	EST3385484 MAGE reassortment, MAGM Homo sapiens cDNA
3522	8683	13830	1.17	2.6E-01	AF233876.1	NT	Danio rerio peptide YY precursor gene, complete cds
3538	8678	13839	6.55	2.6E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 28
3824	8980	14108	1.49	2.6E-01	AJ741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2384780 3'
3824	8980	14108	1.49	2.6E-01	AJ741483.1	EST_HUMAN	wg11c07.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2384780 3'
4043	9174		0.84	2.6E-01	P32323	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4295	9417		0.79	2.6E-01	Q03314	SWISSPROT	RHIB PROTEIN
4714	9830		1.19	2.6E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4721	9835	14970	3.61	2.6E-01	AF007783.1	NT	Chlorostaura fumifera diapausa associated protein 2 (DAP2) mRNA, complete cds
4749	9862	15011	1.58	2.6E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 83 of the complete chromosome
4771	9884		3.4	2.6E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
5203	10300	15437	24.09	2.6E-01	U57838.1	NT	Arabidopsis thaliana FK606 binding protein FKBP62 (ROF-1) gene, complete cds
552	5717	10849	0.74	2.4E-01	AA936316.1	EST_HUMAN	en70d04.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
849	6000	11172	2.06	2.4E-01	BF576124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'
1308	8438	11613	13.62	2.4E-01	AJ289880.1	NT	Homo sapiens KIA08851 gene (partial), X13 gene and LZTFL1 gene
1308	8438	11614	13.62	2.4E-01	AJ289880.1	NT	Homo sapiens KIA08851 gene (partial), X13 gene and LZTFL1 gene
1394	8522	11701	1.03	2.4E-01	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1882	5982		7.18	2.4E-01	AF261753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mktip mRNA, complete cds
1806	7026	12246	0.88	2.4E-01	AF251708.1	NT	Zaocys chumadensis fructose-1,8-bisphosphatase mRNA, complete cds
2242	7353	12810	1.8	2.4E-01	AE000680.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome
2510	7613	12863	1.72	2.4E-01	Z36534.1	NT	D. alscaldum (A3-K) pomA gene
2723	7818	13074	1.33	2.4E-01	X71783.1	NT	S. pombe swi8 gene
2747	7841	13098	3.47	2.4E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
3110	8263		2.69	2.4E-01	U72723.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofl (gag/pol) genes, complete cds
3126	8276	13434	1.77	2.4E-01	X74209.1	NT	H. sapiens AGT gene, PstI fragment of intron 4
3741	8379	14030	0.82	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1685 section 202 of 400 of the complete genome
4004	9137		0.88	2.4E-01	D29860.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
4882	8983	15140	0.08	2.4E-01	BE160080.1	EST_HUMAN	QV4-HT0412-020400-138-b10 HT0412 Homo sapiens cDNA
387	5556	10700	0.87	2.3E-01	S76898.1	NT	aromatase [Poaephila guttata=zabara litchias, ovary, mRNA, 3188 nt]
638	5797		5.1	2.3E-01	U39713.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome

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666	6826	10984	17.78	2.3E-01	U87686.1	NT	Methanococcus jannaschii section 138 of 160 of the complete genome
806	6063	11248	3.03	2.3E-01	BE311883.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1524	6651	11837	1.01	2.3E-01	6877980	NT	Mus musculus vacuolar protein sorting 4b (Vps4b), mRNA
1642	6770	11884	2.22	2.3E-01	Y10887.2	NT	Mus musculus cldf5 gene, exon 1, partial
2039	7166		1.14	2.3E-01	AJ235353.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene
2423	7528	12780	1.37	2.3E-01	BE287718.1	EST_HUMAN	601176562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531016 5'
2612	7711	12864	1.05	2.3E-01	M11318.1	NT	Human erythropoietin gene, complete cds
2784	6823	11702	2.19	2.3E-01	AB016033.1	NT	Methanobacillus agarivorans cyb gene for DNA gyrase subunit B, partial cds, etrainJFO 14857
2832	8086	13263	0.87	2.3E-01	AA801376.1	EST_HUMAN	rep16408.e1 NC1_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu
3056	8209		5.29	2.3E-01	R21732.1	EST_HUMAN	repetitive element contains element THR repetitive element;
3362	8497	13668	0.8	2.3E-01	H68836.1	EST_HUMAN	Y97H10.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:213283 5'
3469	8630	13707	0.84	2.3E-01	4502054	NT	Homo sapiens arachidonate 15-lipoxygenase (ALOX15) mRNA
3818	8955	14103	1.02	2.3E-01	S82821.1	NT	GSTA5=glutathione S-transferase Yc2 subunit (5' region, intron 1) [rat, Morris hepatoma cell line, Genbank, Z212 nt, segment 1 of 3]
3908	9044		6.08	2.3E-01	7682133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4327	9449	14582	0.7	2.3E-01	R82262.1	EST_HUMAN	Y17601.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148017 5'
4378	9500		1.33	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4429	9548	14690	0.7	2.3E-01	D90889.1	NT	Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
4465	9584	14722	2.1	2.3E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4627	9645	14782	6.45	2.3E-01	5031084	NT	Homo sapiens nuclear transport factor 2 (nuclear protein 15) (PP15) mRNA
6053	10155	15288	0.91	2.3E-01	BF316136.1	EST_HUMAN	601896136F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125368 5'
6171	10269	15410	1.05	2.3E-01	AED00240.1	NT	Escherichia coli K-12 MG1655 section 130 of 400 of the complete genome
6195	10282	15429	0.65	2.3E-01	U45324.1	NT	Human Kruppel-related 3 (HKR3) gene, exons 1-3
85	5294	10434	0.72	2.2E-01	A052190.1	EST_HUMAN	cc14610.x1 Soares fetal liver spleen 1NLS S1 Homo sapiens cDNA clone IMAGE:1676280 3' similar to
1680	6708	11900	2.93	2.2E-01	AF187850.1	NT	TR-Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN;
2014	7131		2.57	2.2E-01	AF171801.1	NT	Homo sapiens PPAR delta gene, promoter region
2082	7188	12443	1.53	2.2E-01	M94640.1	NT	Trimerurus malabaricus cyb gene, partial cds; mitochondrial gene for mitochondrial product
2381	7487	12741	2.76	2.2E-01	BF671338.1	EST_HUMAN	Fresh-water sponge Emri alpha collagen (COLF1) gene
2649	7652	12901	1.39	2.2E-01	BE618256.1	EST_HUMAN	602085608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248889 5'
2649	7652	12902	1.39	2.2E-01	BE618256.1	EST_HUMAN	601462628F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868190 5'
2848	8003	13163	4.77	2.2E-01	BE165926.1	EST_HUMAN	601462628F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868190 5'
2848	8003	13164	4.77	2.2E-01	BE155825.1	EST_HUMAN	PM2-HT0363-281299-003-e12 HT0363 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2886	8040		1.5	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphatase hydrolase (FHT) gene, exon 5
3373	8518		2.23	2.2E-01	AL161682.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3761	8828		1.47	2.2E-01	AF155728.1	NT	Xiphophorus maculatus truncated Rax1 retrotransposon reverse transcriptase (RT) pseudogene
4185	9311		0.92	2.2E-01	AF118102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4185	9320	14482	5.31	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcntb) genes, complete cds
4237	9362	14494	2.75	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Mek1) mRNA, complete cds
4237	9362	14495	2.75	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Mek1) mRNA, complete cds
4333	9455	14591	1.02	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4333	9455	14592	1.02	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4477	9597	14736	0.95	2.2E-01	Z54148.1	NT	B. abortus bp28 gene
4784	9807		1.27	2.2E-01	D30004.1	NT	Human beta-cytoplasmic actin (ACTB) pseudogene
4789	9812	15053	3.51	2.2E-01	AA211716.1	EST_HUMAN	z397c05.1r1 Stratiogene INT neuron (5837233) Homo sapiens cDNA clone IMAGE:848688 5'
5025	10127		1.41	2.2E-01	L13289.1	NT	Mus musculus Vinculin gene, exon 3
5099	10169	15338	1.08	2.2E-01	BE141035.1	EST_HUMAN	MR0-HT0087-201099-002-c10 HT0067 Homo sapiens cDNA
5116	10216		0.95	2.2E-01	S57565.1	NT	histamine H2-receptor [rat, Genomic, 1928 nt]
5146	10245	15383	1.83	2.2E-01	4502288	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP6D), nuclear gene encoding mitochondrial protein, mRNA
5184	10291	15428	0.96	2.2E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21G100
5200	10297	15434	1.8	2.2E-01	H60548.1	EST_HUMAN	y42h09.r1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:208001 5' similar to gb214116_ma1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
972	6119	11289	1.38	2.1E-01	AA069289.1	EST_HUMAN	nm31e11.s1 NCL CGAP_Lp2 Homo sapiens cDNA clone IMAGE:1061804
975	6121	11291	0.97	2.1E-01	AL181504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1126	6282		2.76	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 46 of 85 of the complete genome
1201	6334	11503	1.11	2.1E-01	6754298	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1201	6334	11504	1.11	2.1E-01	6754298	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1916	7035	12255	1.16	2.1E-01	AA068824.1	EST_HUMAN	ok73e02.s1 NCL CGAP GC4 Homo sapiens cDNA clone IMAGE:1518610 3' similar to gb:K02765
2199	7253	12499	1.88	2.1E-01	BF065073.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
2880	8044	13208	1.93	2.1E-01	6912445	NT	902083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247603 5'
3785	8922		6.31	2.1E-01	9838381	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
4028	9169	14302	1.27	2.1E-01	P11075	SWISSPROT	Beta vulgaris mitochondrion, complete genome
							IMMEDIATE-EARLY PROTEIN IE180

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4028	9159	14303	1.27	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4356	9477		1.69	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KAA1215 protein, partial cds
4549	9667	14809	2.37	2.1E-01	AB010273.1	NT	Homo sapiens pshsp47 gene, complete cds
5090	10158	15289	1.15	2.1E-01	Q01338	SWISSPROT	ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTOR) (ALPHA-2AAR)
5156	10256		0.88	2.1E-01	AF135027.1	NT	Homo sapiens epsilon acid-binding immunoglobulin-like lectin-8 (SIGLEC8) gene, complete cds
187	5392	10536	1.91	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avens, complete cds
532	5698		2.13	2.0E-01	7705601	NT	Homo sapiens CG1-18 protein (LOC61008), mRNA
697	6854	10958	1.44	2.0E-01	M77085.1	NT	O. cuniculus germline IgH heavy chain V-H pseudogene, alicotype VH2
811	6964	11128	1.69	2.0E-01	AF027865.1	NT	Mus musculus Major Histocompatibility Locus class II region
1012	6165	11321	0.63	2.0E-01	D90905.1	NT	Synschoecysis sp. POC6803 complete genome, 7127, 781449-920816
1126	6263	11427	2.67	2.0E-01	AL169213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1268	6367	11564	1.19	2.0E-01	AJ132695.5	NT	Homo sapiens rac1 gene
1312	6442	11619	1.56	2.0E-01	AW364937.1	EST_HUMAN	PM1-HT0422-281268-002-c08 HT0422 Homo sapiens cDNA
1471	6598		1.61	2.0E-01	AJ243957.1	NT	Pilum pox virus strain M, complete genome, isolate PS
1497	6824	11812	2.89	2.0E-01	4503408	NT	Homo sapiens dysorebrevin, alpha (DTNA), mRNA
1687	6895	11882	4.68	2.0E-01	AB007874.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505
1572	6700	11888	1.65	2.0E-01	AF280700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1710	6838	12039	1.27	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (bradyk1) gene, complete cds
1732	6859		1.48	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 jagged2 gene, complete cds, and unknown gene
1769	6895		2.1	2.0E-01	U87625.1	NT	Methanococcus jannaschii section 87 of 150 of the complete genome
1897	7016	12236	1.08	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE3853330 5'
1897	7016	12237	1.08	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE3853330 5'
2327	7436		1.03	2.0E-01	X82877.1	NT	H. sapiens Nar-D-glucose cotransport regulator gene
3558	8696		0.84	2.0E-01	AW238005.1	EST_HUMAN	Yp1502Lx1 NCL CGAP_HIN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element
3684	8823	13979	0.84	2.0E-01	P34641	SWISSPROT	MER21 repetitive element;
3689	8828		0.71	2.0E-01	6680797	NT	GED-11 PROTEIN
3927	9053	14221	0.63	2.0E-01	Z48008.1	NT	Mus musculus bone morphogenetic protein 8 (Bmp8), mRNA
4003	9138	14276	0.76	2.0E-01	X83397.1	NT	Sus scrofa
4409	9529	14669	0.74	2.0E-01	AF242431.1	NT	C. parvifolia eapC gene
4538	9596		7.82	2.0E-01	BE826165.1	EST_HUMAN	Mus musculus neuronal apoptosis inhibitory protein 8 (Nai8) gene, complete cds, and Nai3 gene, exon 2-9 and 11-16
5022	10124	15256	5.96	2.0E-01	8922080	NT	QV4-EN0032-180500-223-c03 EN0032 Homo sapiens cDNA
5087	10187	15326	0.98	2.0E-01	Y18216.1	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
							Homo sapiens putative pailHbD pseudogene for hair keratin, exons 1 to 9

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5169	10287	15408	48.35	2.0E-01	Y14980.1	NT	<i>Adrenomedullin</i> fur gene
106	6310		7.75	1.9E-01	7549743	NT	<i>Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahr1)</i> , mRNA
349	5522	10871	4.93	1.9E-01	AF004353.1	NT	<i>Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds</i>
655	5916	10953	1.43	1.9E-01	U92581.2	NT	<i>Homo sapiens lamda/ota protein kinase C-interacting protein mRNA, complete cds</i>
655	5816	10954	1.43	1.9E-01	U32581.2	NT	<i>Homo sapiens lamda/ota protein kinase C-interacting protein mRNA, complete cds</i>
662	5823	10951	5.59	1.9E-01	BE070801.1	EST_HUMAN	<i>RC3-BT0502-251169-011-401 BT0502 Homo sapiens cDNA</i>
663	5823	10951	4.32	1.9E-01	BE070801.1	EST_HUMAN	<i>RC3-BT0502-251169-011-401 BT0502 Homo sapiens cDNA</i>
987	6133		1.34	1.9E-01	7306180	NT	<i>Mus musculus Interleukin 2 receptor, gamma chain (IL2rg)</i> , mRNA
1105	6243	11407	7.57	1.9E-01	AA35813.1	EST_HUMAN	<i>EST07784 Fetal Lung II Homo sapiens cDNA 5' end</i>
1378	6507	11688	1.76	1.9E-01	AF061282.1	NT	<i>Sorghum bicolor 22 kDa kafirin cluster</i>
1445	6573		2.28	1.9E-01	AF184623.1	NT	<i>Plasmodium vivax reticulocyte binding protein-2 (rpb-2) gene, complete cds</i>
2381	7468	12723	1.77	1.9E-01	8922533	NT	<i>Homo sapiens hypothetical protein FLJ10581 (FLJ10581)</i> , mRNA
2888	8042	13206	4.43	1.9E-01	U83038.1	NT	<i>Sigmoidon hispidus p53 gene, partial cds</i>
2904	8057		5.64	1.9E-01	J00922.1	NT	<i>Gallus gallus ovalbumin (Y) gene, complete cds</i>
2872	8126	13290	0.97	1.9E-01	U25148.1	NT	<i>Rattus norvegicus brush border myosin-4 (BBM4)</i> , mRNA, partial cds
3376	8321	13685	3.57	1.9E-01	D13197.1	NT	<i>Mouse gene for immunoglobulin diversity region D1</i>
3461	8603	13787	4.34	1.9E-01	R16467.1	EST_HUMAN	<i>y42f10.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:128647 6'</i>
3783	8920	14071	0.77	1.9E-01	AF284017.1	NT	<i>Rattus norvegicus arylacetamide deacetylase gene, complete cds</i>
3987	9102	14250	4.13	1.9E-01	AB006784.1	NT	<i>Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds</i>
4060	9191	14332	1.39	1.9E-01	AW754106.1	EST_HUMAN	<i>CUG-CT0315-271169-045-b11 CT0315 Homo sapiens cDNA</i>
4209	9334	14466	1.02	1.9E-01	BE834943.1	EST_HUMAN	<i>MRI-FN0010-280700-007-004 FN0010 Homo sapiens cDNA</i>
4448	9587	14708	0.98	1.9E-01	AL161483.2	NT	<i>Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5</i>
4988	10104		0.98	1.9E-01	AF223642.1	NT	<i>Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds</i>
90	5241	10357	2.04	1.8E-01	U73200.1	NT	<i>Mus musculus p116Rip mRNA, complete cds</i>
257	7887	10696	1.87	1.8E-01	AB022090.1	NT	<i>Mus musculus Ceb gene for chaperonin containing TCP-1 gamma subunit, partial cds</i>
368	5648	10692	1.14	1.8E-01	4802692	NT	<i>Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2)</i> , mRNA, and translated products
745	5901	11055	0.7	1.8E-01	AB021490.2	NT	<i>Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds</i>
983	8129	11297	0.69	1.8E-01	AB12212.1	EST_HUMAN	<i>w47102.x1 NC1 CGAP Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'</i>
1092	8230	11394	1.22	1.8E-01	AF000580.1	NT	<i>Dicystosium discoidium plasmid Ddp5, complete genome</i>
1292	6421	11596	5.06	1.8E-01	AL117189.1	NT	<i>Yersinia pestis plasmid pCD1</i>
1518	6845	11831	1.83	1.8E-01	6753947	NT	<i>Mus musculus guanylate nucleotide binding protein 1 (Gbp1)</i> , mRNA
1518	6845	11832	1.83	1.8E-01	6753947	NT	<i>Mus musculus guanylate nucleotide binding protein 1 (Gbp1)</i> , mRNA
1858	6976		1.09	1.8E-01	4505036	NT	<i>Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4)</i> , mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1877	6997		1.21	1.8E-01	AI733708.1	EST_HUMAN	gq22d10.x5 NCI_CGAP_K43 Homo sapiens cDNA clone IMAGE:1761611 3' similar to TR:O75938 O75938 GAMMA BUTYROBETAINE HYDROXYLASE;
1918	7037	12257	1.29	1.8E-01	AB051897.1	NT	Mus musculus Scya8, Scya9, Scya16-pa, Scya5 genes for small inducible cytokine A8 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2863	7761		1.44	1.8E-01	AW935728.1	EST_HUMAN	QV3-DT0018-081289-039-g04 DT0018 Homo sapiens cDNA
2863	8018		1.78	1.8E-01	AF184589.1	NT	Jonopsidium scales LEAFY protein (LEAFY2) gene, partial cds
2868	8022	13189	1.54	1.8E-01	AW182800.1	EST_HUMAN	Y41a03.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2658768 3'
3101	8264	13404	2.1	1.8E-01	AW995178.1	EST_HUMAN	QV0-BN0047-070300-147-c04 BN0041 Homo sapiens cDNA
3348	8493	13660	0.63	1.8E-01	BF183582.1	EST_HUMAN	601809723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040621 3'
3604	8743	13897	0.79	1.8E-01	HC3369.1	EST_HUMAN	Y4501.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
3604	8743	13898	0.79	1.8E-01	HC3369.1	EST_HUMAN	Y4501.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
4309	8431		0.89	1.8E-01	D37894.1	NT	Bovine NB25 mRNA for MHC class II (BcLA-DQB), complete cds
4528	8847	14768	6.51	1.8E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4738	8861	14998	2.65	1.8E-01	AB051897.1	NT	Mus musculus Scya8, Scya9, Scya16-pa, Scya5 genes for small inducible cytokine A8 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
4774	8887	15033	1.06	1.8E-01	X62178.1	NT	S.tuberosum mRNA for alcohol dehydrogenase
4837	9949	15093	50.8	1.8E-01	AA383750.1	EST_HUMAN	ES187196 Testis 1 Homo sapiens cDNA 5' end
5027	10126	15258	1.83	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151289-112-g06 ST0203 Homo sapiens cDNA
5041	10143	15273	0.68	1.8E-01	AI792382.1	EST_HUMAN	an28g07.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700028 5'
5079	10180	15316	10.32	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5092	10192	15332	0.81	1.8E-01	AI439891.1	EST_HUMAN	i167a04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'
5133	10233	15388	11.74	1.8E-01	AJ132844.1	NT	Broad bean wilt virus 2 genes encoding 118kDa protein, 104kDa protein, large coat protein, small coat protein
5193	10233	15370	11.74	1.8E-01	AJ132844.1	NT	Broad bean wilt virus 2 genes encoding 118kDa protein, 104kDa protein, large coat protein, small coat protein
576	5739	10636	1.03	1.7E-01	BE385184.1	EST_HUMAN	80127490-4F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3815788 5'
808	5959	11122	2.09	1.7E-01	X63350.1	NT	P.dumetii histone gene cluster for core histones H2A, H2B, H3 and H4
662	6110		1.5	1.7E-01	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1983	7100		1.85	1.7E-01	AF256051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2823	7979	13138	2.4	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapt) gene, complete cds, and YRAL VIBCO gene, partial cds
2823	7979	13138	2.4	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapt) gene, complete cds, and YRAL VIBCO gene, partial cds
2823	8046	13211	1.38	1.7E-01	AA336809.1	EST_HUMAN	EST141851 Endometrial tumor Homo sapiens cDNA 5' end
2865	8119	13282	1.14	1.7E-01	AJ238738.1	NT	Naja naja atra ctk-1 gene, exons 1-3
2865	8119	13283	1.14	1.7E-01	AJ238738.1	NT	Naja naja atra ctk-1 gene, exons 1-3
3081	8234	13384	1.81	1.7E-01	AF081614.1	NT	Tetrahodon geryanigeryanil diphosphate synthase mRNA, complete cds
3347	8482	13659	0.81	1.7E-01	N56763.1	EST_HUMAN	J2346F Human fetal heart Lambda ZAP Expressa Homo sapiens cDNA clone J2346 5'
3428	8570	13730	1.32	1.7E-01	AJ268505.1	NT	Arabidopsis sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
3911	9047	14208	5.39	1.7E-01	AJ283771.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL-PRX gene fused to intron 5 of the AF-4/FEL gene
4533	8851		1.76	1.7E-01	X62836.1	NT	Schistosoma gregaria alpha repetitive DNA
4806	8918	15039	1.16	1.7E-01	AI247635.1	EST_HUMAN	q157d09.x1 Scaree2_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 ORF repetitive element
5103	10204		1.17	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme 1b (se) gene, complete cds
5138	10238	15374	0.82	1.7E-01	BF030010.1	EST_HUMAN	601557259F1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3827187 5'
121	5321	10485	1.23	1.8E-01	AF217632.1	NT	Homo sapiens mevalonate kinase gene, exon 6 and 7
678	7885	10978	1.15	1.6E-01	R31497.1	EST_HUMAN	Y476F12.1 Scaree2 placenta NB2HP Homo sapiens cDNA clone IMAGE:185589 5'
1519	6848	11833	1.19	1.6E-01	AA546863.1	EST_HUMAN	nk28d12.e1 NCL_CGAP_Cot11 Homo sapiens cDNA clone IMAGE:1014839 3'
1537	6884	11850	3.14	1.6E-01	AF298117.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1829	7048	12289	1.14	1.6E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2363	7839	12725	1.35	1.8E-01	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
2385	7491	12744	1.94	1.6E-01	AF161633.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 33
2858	8013	13178	33.76	1.6E-01	AF165589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2858	8013	13177	33.76	1.6E-01	AF165589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3613	8752	13908	1.03	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
3613	8752	13908	1.03	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
3976	9109		2.81	1.6E-01	AE004413.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome
4305	9427	14592	10.51	1.6E-01	AF178980.1	NT	Homo sapiens apelin gene, complete cds
4435	9554		2.91	1.6E-01	AW988601.1	EST_HUMAN	EST380877 MAGE resequences, MAGJ Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4443	8592		4.45	1.6E-01	6753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
4822	10032	15173	1.22	1.6E-01	AA088343.1	EST_HUMAN	z84409.e1 Stragene colon (#837204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TRE221955
4852	10060	15168	1.54	1.6E-01	AJ006356.1	NT	E221955 38,855 BP SEGMENT OF CHROMOSOME XIV. ;
4852	10060	15169	1.54	1.6E-01	AJ006358.1	NT	Lycopodium obscurum Real fragment 2, satellite region
5101	10201	15339	1.02	1.6E-01	AL333984.1	EST_HUMAN	Lycopodium obscurum Real fragment 2, satellite region
5101	10201	15340	1.02	1.6E-01	AL333984.1	EST_HUMAN	DKFZp434O1729_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434O1729 5'
5186	10283	15420	0.97	1.6E-01	AL161842.2	NT	DKFZp434O1729_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434O1729 5'
245	6436	10575	1.59	1.5E-01	BE710087.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
245	6436	10576	1.59	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-187-E05 HT0619 Homo sapiens cDNA
385	7894		2.03	1.5E-01	AV711688.1	EST_HUMAN	IL3-HT0619-040700-187-E05 HT0619 Homo sapiens cDNA
783	5938	11096	1.83	1.5E-01	AL163284.2	NT	AV711688 DCA Homo sapiens cDNA clone DCAADH08 5'
1063	6231	11395	0.84	1.5E-01	AJ009755.1	NT	Homo sapiens chromosome 21 segment HS21C084
1098	6236	11399	2.29	1.5E-01	AJ281885.1	NT	Gyathus carpio mRNA for EGG522 myosin heavy chain, 3'UTR
1114	6262		1.53	1.5E-01	L36125.1	NT	Homo sapiens partial SLG22A2 gene for organic cation transporter (OCT2), exon 1
1218	6351	11520	1.03	1.5E-01	AW186516.1	EST_HUMAN	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1278	6408	11582	3.97	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1278	6408	11583	3.97	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-16)
1492	6619	11809	1.88	1.6E-01	AF117340.1	NT	Mus musculus MAP kinase kinase 1 (Mekk1) mRNA, complete cds
2878	8033		1.18	1.6E-01	AW672516.1	EST_HUMAN	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
3007	8161	13318	0.88	1.6E-01	MB1441.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-16)
3334	8480	13846	4.18	1.5E-01	AA935049.1	EST_HUMAN	Mus musculus MAP kinase kinase 1 (Mekk1) mRNA, complete cds
3350	8485	13863	0.61	1.6E-01	Z23104.1	NT	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);
3350	8485	13864	0.61	1.6E-01	Z23104.1	NT	Boa laurus factor V variant 2 (factor V) mRNA, complete cds
3738	8874	14025	2.53	1.5E-01	U06984.1	NT	RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN);
3752	8889	14040	1.34	1.5E-01		NT	L. stagnalis mRNA for G protein-coupled receptor
3848	8982	14137	2.23	1.5E-01	AW665983.1	EST_HUMAN	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
4024	9156	14300	0.88	1.5E-01	AW368650.1	EST_HUMAN	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
4154	9280	14418	6.53	1.5E-01	AL163284.2	NT	h10106.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2881411 3'
4893	9809	14956	1.55	1.5E-01	BF687605.1	EST_HUMAN	RC2-HT0149-191099-012-c09 HT0149 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C084
							602067192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066223 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4716	7769	13021	2.25	1.6E-01	BF69381.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
4758	9871	15021	1.18	1.6E-01	BE173786.1	EST_HUMAN	CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4759	9871	15022	1.18	1.6E-01	BE173786.1	EST_HUMAN	CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4985	10093	16224	1.21	1.5E-01	AL181580.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
287	5485		0.88	1.4E-01	AF000683.1	NT	Homo sapiens T cell receptor beta locus, TCRBV8S9P to TCRBV21S2A2 region
811	6051		2.65	1.4E-01	D78838.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1263	6382		2.4	1.4E-01	T01894.1	EST_HUMAN	yd64c01.s1 Soares fetal liver spleen 1N1FS Homo sapiens cDNA clone IMAGE:112032 3'
1760	6886		1.38	1.4E-01	6078880	NT	Mus musculus growth differentiation factor 6 (Gdf6), mRNA
1763	6889	12095	1.83	1.4E-01	AE001710.1	NT	Thermoboga maritima section 22 of 138 of the complete genome
1986	7103		8.52	1.4E-01	AA720815.1	EST_HUMAN	ny72607.s1 NCI_CGAP_G031 Homo sapiens cDNA clone IMAGE:1283821 3'
2763	7847	13103	2.03	1.4E-01	AI933408.1	EST_HUMAN	wm74401.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441685 3'
3876	8011	14187	1	1.4E-01	R59292.1	EST_HUMAN	y97403.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:41467 5'
3876	8011	14188	1	1.4E-01	R59292.1	EST_HUMAN	y97403.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:41467 5'
4145	8273	14410	8.95	1.4E-01	AI698094.1	EST_HUMAN	b366c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4145	8273	14411	8.95	1.4E-01	AI698094.1	EST_HUMAN	b366c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4216	8340	14472	3.21	1.4E-01	AE001710.1	NT	Thermoboga maritima section 22 of 138 of the complete genome
4848	8798	14911	0.76	1.4E-01	5453881	NT	Homo sapiens phosphodiesterase 4A, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E2) (PDE4A), mRNA
320	5508	10844	1.71	1.3E-01	4758487	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
320	5508	10845	1.71	1.3E-01	4758487	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
527	5693	10826	2.26	1.3E-01	AB013199.1	NT	Homo sapiens gene for NBS1, complete cds
639	5798	10930	0.94	1.3E-01	AJ277606.1	NT	Human calicivirus HUJNLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUJNLV/Girlington/83/UK
639	5798	10931	0.94	1.3E-01	AJ277606.1	NT	Human calicivirus HUJNLV/Girlington/83/UK RNA for capsid protein (ORF2), strain HUJNLV/Girlington/83/UK
845	5998	11187	0.82	1.3E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
895	6046	11216	1.34	1.3E-01	AF139818.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1028	6169	11334	1.59	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1128	6265		2.22	1.3E-01	AL115285.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1218	6350	11519	2.48	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAF05 5'
1465	6582		0.98	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CHS mRNA, complete cds
1863	7080	12304	1.49	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2267	7377		1.09	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191089-032-012 ST0173 Homo sapiens cDNA
2360	7467		1.82	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 81 of 172 of the complete genome

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2548	7651	12800	1.78	1.3E-01	M86918.1	NT	Caressius aureatus keratin type I mRNA, complete cds
3338	8484	13850	1.12	1.3E-01	AF198779.1	NT	Homo sapiens transcription factor 1GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α_2
3482	8574	13734	0.9	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydroxyoloyl transacylase mRNA, complete cds
3702	8840	13894	1.39	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt position (177)
3702	8840	13895	1.39	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt position (177)
3709	8847	14001	0.7	1.3E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydrodiol dehydrogenase 4 [AKR 1C4], exon 2
3781	8918	14069	0.67	1.3E-01	6978840	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA
3963	9098		1.48	1.3E-01	AL161681.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4025	5796	10830	0.77	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/83AUK RNA for capsid protein (ORF2), strain HUNLV/Girlington/83AUK
4025	5796	10831	0.77	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/83AUK RNA for capsid protein (ORF2), strain HUNLV/Girlington/83AUK
4109	9237		1.01	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4130	9258		3.02	1.3E-01	AW384341.1	EST_HUMAN	QV3-DT0018-081289-038-c03 DT0018 Homo sapiens cDNA
4137	9265	14404	1.97	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4157	9283	14419	17.18	1.3E-01	AW273741.1	EST_HUMAN	KV23F10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813895 3'
4264	9388	14526	1.08	1.3E-01	AV752278.1	EST_HUMAN	AV752278 NPJ Homo sapiens cDNA clone NPJAZE02 6'
4264	9389	14527	1.08	1.3E-01	AV752278.1	EST_HUMAN	AV752278 NPJ Homo sapiens cDNA clone NPJAZE02 6'
4291	9418		1.43	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4458	9577	14715	0.69	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydroxyoloyl transacylase mRNA, complete cds
4508	9627	14770	2.33	1.3E-01	BE272338.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890083 6'
4915	10025		0.97	1.3E-01	Y12684.1	NT	H. Leptospira gene encoding translin, exon 3
381	6590	10735	12.88	1.2E-01	AK421744.1	EST_HUMAN	IF89b02.x1 NCL_OGAP_Bm23 Homo sapiens cDNA clone IMAGE:2098538 3' similar to gb:U05760_mai1
423	6710		1.77	1.2E-01	U68912.1	NT	ANNEXIN V (HUMAN);
548	6711		2.49	1.2E-01	AF039442.1	NT	Dicystosialum discobolium ORF DG1016 gene, partial cds
1366	6614	11693	2.43	1.2E-01	AU149146.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1366	6514	11693	2.43	1.2E-01	AU149146.1	EST_HUMAN	AU149148 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1393	6621		2.74	1.2E-01	AV735249.1	EST_HUMAN	AU149148 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1622	6649		1.04	1.2E-01	AA897474.1	EST_HUMAN	AV735249 cda Homo sapiens cDNA clone cdaAAJB11 5'
							af48e09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1480584 3' similar to TRCQ16971
							Q16871 ANTHAMULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR.;

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1641	6769	11883	1.4	1.2E-01	Q14834	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3)
1653	6781	11887	2.95	1.2E-01	AI295402.1	EST_HUMAN	q689709.x1 NCL_CGAP_Esc2 Homo sapiens cDNA clone IMAGE:1868563 3'
1770	6905		8.41	1.2E-01	X69211.1	NT	H. sapiens DNA for endogenous retroviral like element
1823	7042		3.35	1.2E-01	AW449388.1	EST_HUMAN	UI-H-B13-ak-e-10-Q-UJ.at NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734594 3'
2184	7277	12824	1.94	1.2E-01	BF248480.1	EST_HUMAN	601821587F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4048224 5'
2551	7654	12804	2.16	1.2E-01	AW888598.1	EST_HUMAN	QY3-BN0046-220300-129-F10 BN0048 Homo sapiens cDNA
2557	7659	12812	10.83	1.2E-01	BE219889.1	EST_HUMAN	HW6504.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3178303 3'
2805	7881	13124	1.36	1.2E-01	U18018.1	NT	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
2887	8021	13188	2.04	1.2E-01	AI720470.1	EST_HUMAN	es80c09.x1 Barstead codon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:U05095
2890	8054	13223	3.27	1.2E-01	M18364.1	NT	60S RIBOSOMAL PROTEIN L30 (HUMAN);
2876	8130	13284	0.74	1.2E-01	X56882.1	NT	Human creatine kinase-B mRNA, complete cds
3215	8388	13930	1.77	1.2E-01	AW370688.1	EST_HUMAN	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3240	8390		0.72	1.2E-01	U87600.1	NT	QV1-BT0258-261089-021-405 BT0258 Homo sapiens cDNA
3490	8602		0.81	1.2E-01	Z69118.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3507	8848	13814	1.26	1.2E-01	X56882.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
3607	8948	13816	1.25	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3691	8802		0.84	1.2E-01	Z69118.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3750	8887		0.78	1.2E-01	BF128551.1	EST_HUMAN	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
4163	9278	14414	1.91	1.2E-01	Z54255.1	NT	601810788R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053688 3'
4163	9278	14416	1.91	1.2E-01	Z54255.1	NT	P. clarkii mRNA; repeat region (ID 2MR17)
4739	8852		2.5	1.2E-01	L32873.1	NT	P. clarkii mRNA; repeat region (ID 2MR17)
5026	10131	15260	1	1.2E-01	BE173168.1	EST_HUMAN	Arabidopsis thaliana homeodomain protein (GLABRA2) gene, complete cds
5028	10131	15261	1	1.2E-01	BE173168.1	EST_HUMAN	MRO-HT0559-240400-018-c09 HT0559 Homo sapiens cDNA
5063	10165		1.01	1.2E-01	P16468	SWISSPROT	MRO-HT0559-240400-018-c09 HT0559 Homo sapiens cDNA
5663	6728	10868	0.7	1.1E-01	AI561003.1	EST_HUMAN	HEMOLYSIN PRECURSOR
612	5772	10902	2.13	1.1E-01	AA69006.1	EST_HUMAN	tr18d08.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2187883 3'
1056	6197	11362	1.37	1.1E-01	BF887308.1	EST_HUMAN	trm08g11.x1 NCL_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X06885_ma1
1088	6225		1.4	1.1E-01	AL161560.2	NT	HEME OXYGENASE 1 (HUMAN);
1161	7810	11482	3.63	1.1E-01	AW672168.1	EST_HUMAN	602129847F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:4286771 5'
1253	6383	11561	1.31	1.1E-01	DB4004.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1535	6682	11848	2.07	1.1E-01	AI140363.1	EST_HUMAN	EST1354142 MAGE resequences, MAGL Homo sapiens cDNA
							Synechocystis sp. PCC6803 complete genome, 23/27, 2888/67-3002865
							AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2292	7401		1.57	1.1E-01	8766216	NT	Mus musculus pre T-cell antigen receptor alpha (Ptau), mRNA
2818	7874	13133	1.1	1.1E-01	S82418.1	NT	Interleukin-12 p35 subunit [mice, Genbank, 700 nt, segment 4 of 5]
3005	8159	13316	0.89	1.1E-01	F03285.1	EST_HUMAN	HSC1RF022, normalized infant brain cDNA Homo sapiens cDNA clone o-1r02 3'
3328	8470		1.44	1.1E-01	8753231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Ca α 1g), mRNA
3402	8546	13705	2.31	1.1E-01	BE363186.1	EST_HUMAN	601308670F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627068 5'
3433	9575	13735	1.36	1.1E-01	X62185.1	NT	C. reinhardtii nuclear gene on linkage group XX
3472	8614	13781	0.63	1.1E-01	R88948.1	EST_HUMAN	Y60208.a1 Scarsa fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:200414 3' similar to contains
3570	8711	13871	0.76	1.1E-01	Y07695.1	NT	Alu repetitive element
3687	8828	13981	1.31	1.1E-01	X52708.1	NT	A. Jimmerus gene for transposase
4086	9216	14348	0.85	1.1E-01	AW819412.1	EST_HUMAN	G. gallus gene encoding non-Histone chromosomal protein HMG-14b, exons 4 and 5
4086	9216	14349	0.85	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-280100-025-g07 ST0280 Homo sapiens cDNA
4226	9354		7.73	1.1E-01	AF167066.1	NT	MR3-ST0280-280100-025-g07 ST0280 Homo sapiens cDNA
4281	9386	14523	0.65	1.1E-01	AW802036.1	EST_HUMAN	Drosophila melanogaster Klaricht protein (Klar) mRNA, complete cds
4800	9813	15064	1.32	1.1E-01	Y07695.1	NT	13-JUN070-020500-088-a08 UN0070 Homo sapiens cDNA
							A. Jimmerus gene for transposase
5008	9219		0.6	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysochalcidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tansach X (TNX) genes, complete
1204	5337		3.9	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1276	6406	11579	2.88	1.0E-01	A1985498.1	EST_HUMAN	w508001.x1 NCL CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.B
1399	6327	11706	1.81	1.0E-01	AL161604.2	NT	MER7 repetitive element
3498	8639	13805	1.03	1.0E-01	BF033591.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
3639	8837	13891	0.92	1.0E-01	BF239818.1	EST_HUMAN	601456301F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3859949 5'
3813	8850	14097	0.98	1.0E-01	AF287061.1	NT	601908489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 6'
3813	8950	14098	0.98	1.0E-01	AF287061.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
3828	9062	14220	2.33	1.0E-01	BF365703.1	EST_HUMAN	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
4628	8848		0.61	1.0E-01	A1792349.1	EST_HUMAN	QV2-NT0048-160800-318-e05 NT0048 Homo sapiens cDNA
4880	8786	14941	1.02	1.0E-01	U50450.1	NT	an3204.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4903	10013	15157	2.26	1.0E-01	AW952344.1	EST_HUMAN	Drosophila melanogaster tyrosine kinase p45 isoform (lar) mRNA, complete cds
5106	10207	16344	1.08	1.0E-01	AL163279.2	NT	EST38-4114 MAGE resequences, MAGEB Homo sapiens cDNA
							Homo sapiens chromosome 21 segment H321C079
2739	7833	13086	0.95	9.8E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-R1) mRNA, complete cds
2748	7842	13097	1.36	8.8E-02	BE45554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456385 5'

Table 4 :

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2748	7842	13088	1.36	9.9E-02	BE545594.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
3249	8389	13560	1.23	9.9E-02	AF09810.1	NT	Homo sapiens neurodin III-alpha gene, partial cds
562	5727		1.69	9.8E-02	X56338.1	NT	O. sativa RAmY3C gene for alpha-amyrase
3078	8231		1.57	9.8E-02	4504578	NT	Homo sapiens I factor (complement) (IF) mRNA
3123	8275	13430	3.74	9.8E-02	AF184274.1	NT	Daucus carota leucanthocyranidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4201	8326	14457	6.41	9.8E-02	AF257329.1	NT	Lepidoptera maculata beta-tubulin mRNA, complete cds
4201	8326	14458	6.41	9.8E-02	AF257328.1	NT	Lepidoptera maculata beta-tubulin mRNA, complete cds
1367	8486	11687	1.12	9.7E-02	AB003808.1	NT	Aloe arborescens mRNA for NADP-malic enzyme, complete cds
2241	7352	12609	1.38	9.7E-02	BE108680.1	EST_HUMAN	QV1-HT0516-070300-095-e04 HT0516 Homo sapiens cDNA
3968	8081		3.91	9.7E-02	Q89795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
4322	9444	14577	3.44	9.6E-02	Z33888.2	NT	Proteus mirabilis fibrinolytic operon, strain HI4320
4987	10094	16225	1.27	9.6E-02	AW66820.1	EST_HUMAN	EST178303 MAGE resequences, MAGI Homo sapiens cDNA
4077	8207	14344	1.88	9.6E-02	AW892365.1	EST_HUMAN	GM2-BN0023-050200-087-F12 BN0023 Homo sapiens cDNA
1847	8938	12188	2.28	9.4E-02	BF071083.1	EST_HUMAN	602150802F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291617 5'
3858	8394	14151	5.14	9.4E-02	Z33059.1	NT	M. capricornum MAGE resequences, MAGI Homo sapiens cDNA
2858	8112		1.78	9.3E-02	4809280	NT	M. capricornum MAGE resequences, MAGI Homo sapiens cDNA
3000	8155		6.69	9.3E-02	6912625	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
3239	8389	13552	1.84	9.3E-02	BF575511.1	EST_HUMAN	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
4124	8252	14389	3.24	9.3E-02	BE391843.1	EST_HUMAN	602193308F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4124	8252	14380	3.24	9.3E-02	BE391843.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607853 5'
4703	8319		1.91	9.3E-02	AV732224.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607853 5'
227	5421	10559	7.03	9.2E-02	U60315.1	NT	AV732224 HTF Homo sapiens cDNA clone HTFAU08 5'
227	5421	10557	7.03	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
227	5421	10558	7.03	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2209	7321		5.16	9.2E-02	R84158.1	EST_HUMAN	Molluscum contagiosum virus subtype 1, complete genome
3159	8310	13470	9.52	9.2E-02	Q28631	SWISSPROT	Y98807.1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:41618 5'
3287	8436	13587	0.82	9.2E-02	AA534384.1	EST_HUMAN	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3573	8714		1.06	9.2E-02	6755215	NT	HT78d01.s1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:828138 3'
4216	8341		0.94	9.2E-02	U82048.1	NT	Mus musculus pre T-cell antigen receptor alpha (Pctra), mRNA
4285	9407		0.76	9.2E-02	BE298722.1	EST_HUMAN	Human herpesvirus 1 strain KOS-83, latency-associated transcript, promoter region
4808	9728	14882	1.22	9.2E-02	X98402.1	NT	600844385F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2880178 5'
422	5209	10322	1.78	9.1E-02	X77685.1	NT	O. cuniculus K12 keratin gene
2391	7497	12749	2.69	9.1E-02	P78986	SWISSPROT	O. cuniculus K12 keratin gene
3847	8788		0.94	9.1E-02	AW372568.1	EST_HUMAN	6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE)
							PM2-BT0349-181298-001-f02 BT0349 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4463	9592	14720	1.35	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
743	5899	11052	5.28	9.0E-02	P15328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1845	6773	11985	4.28	9.0E-02	BE220482.1	EST_HUMAN	h39g10.x1 NC1 CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175942 3' similar to contains Alu repetitive element
2764	7859	13114	2.63	9.0E-02	AF138522.1	NT	HIV-1 p8c085-08 from USA envelope glycoprotein (env) gene, partial cds
2784	7898	13115	2.63	9.0E-02	AF138522.1	NT	HIV-1 p8c085-08 from USA envelope glycoprotein (env) gene, partial cds
3318	8465	13628	1.42	9.0E-02	AF279135.1	NT	Dicystosium discoidium spore coat structural protein SP65 (ooc) gene, complete cds
4275	9398	14538	0.61	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Salimiri scireus-squirrel monkey, liver, mRNA, 1474 nt]
4276	9398	14539	0.61	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Salimiri scireus-squirrel monkey, liver, mRNA, 1474 nt]
4398	9516	14699	0.97	9.0E-02	P65268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (SLAMININ)
4638	9759	14803	2.02	9.0E-02	X65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
1448	6576	11762	2.13	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285951 5'
1448	6576	11763	2.13	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4285951 5'
4171	9297		1.62	8.9E-02	AF269055.1	NT	Atrichum angustatum AtranFia2 protein (AtranFia2) gene, partial cds
4604	9722	14858	1.02	8.9E-02	AA424887.1	EST_HUMAN	zwc3404.s1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:768189 3'
1382	6510	11691	1.57	8.8E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3880	9016	14173	0.99	8.8E-02	AA289128.1	EST_HUMAN	EST11695 Uterus Homo sapiens cDNA 5' end
							TRANSCRIPTION INITIATION FACTOR TFIID 139 KDA SUBUNIT (TAFII139) (TAFII-130) (TAFII130)
4008	9141		3.08	8.8E-02	O00268	SWISSPROT	Homo sapiens chromogranin A (parathyroid secretory protein 1) (CHGA) mRNA
4217	6342		1.07	8.8E-02	4502804	NT	Homo sapiens paired box gene 8 (enlidia, kenafilia) (PAX8), isoform b, mRNA
4278	9401		0.76	8.8E-02	4580423	NT	Homo sapiens paired box gene 8 (enlidia, kenafilia) (PAX8), isoform b, mRNA
1659	6787	11982	1.11	8.7E-02	AI187281.1	EST_HUMAN	α65b01.s1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:1681161 3'
3670	8809	13988	4.16	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3670	8809	13987	4.16	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4874	9790	14938	1.39	8.7E-02	AF178938.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
1268	6395	11582	5.55	8.6E-02	AL271738.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
2224	7336	12590	1.27	8.6E-02	BE408897.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 22
3170	8321	13482	3.62	8.6E-02	U05468.1	NT	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638943 5'
							Tichoneres vaginella beta-tubulin (btub1) gene, complete cds

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3822	8761		3.68	8.6E-02	AF153382.1	NT	Dicystostellum discoideum adenyl cyclase (acaA) gene, complete cds
8135	10235	15371	2.2	8.6E-02	AF080774.1	NT	Rattus norvegicus synaptic vesicle protein 2C (SV2C) mRNA, complete cds
2373	7479	12733	1.4	8.6E-02	AE000852.1	NT	Helicobacter pylori 268958 section 130 of 134 of the complete genome
2828	7947	12981	2.91	8.4E-02	W60330.1	EST_HUMAN	z444611.1 Soares fetal heart_Nb1H119W Homo sapiens cDNA clone IMAGE:343532 5'
4331	9453	14587	0.95	8.4E-02	AF267213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
4331	9453	14588	0.95	8.4E-02	AF267213.1	NT	Cavia porcellus glycoprotein alpha-subunit mRNA, complete cds
3579	8720	13878	0.98	8.3E-02	P76334	SWISSPROT	HYPOTHETICAL LIPOPROTEIN MG308 HOMOLOG PRECURSOR
1389	6517		4.18	8.2E-02	Y08170.2	NT	Gallus gallus mRNA for for OBCAM protein gamma isoform
1609	6536	11823	2.08	8.2E-02	AF167077.2	NT	Canis familiaris glutamate transporter (EAA14) mRNA, complete cds
3045	8189		2.21	8.2E-02	AL163205.2	NT	Homo sapiens chromosome 21 segment HS21C006
3780	8917		1.32	8.2E-02	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3982	9116	14204	1.16	8.2E-02	AL163205.2	NT	Homo sapiens chromosome 21 segment HS21C006
4258	9383	14518	5.8	8.2E-02	P48900	SWISSPROT	LEUCOCYTE ANTIGEN CD87 PRECURSOR
4268	9383	14517	5.8	8.2E-02	P48900	SWISSPROT	LEUCOCYTE ANTIGEN CD87 PRECURSOR
4268	9383	14518	5.8	8.2E-02	P48900	SWISSPROT	LEUCOCYTE ANTIGEN CD87 PRECURSOR
6050	10152	15283	0.67	8.2E-02	AF240778.1	NT	Mus musculus peptidogen F (Pepf) mRNA, complete cds
6066	10167	15301	3.12	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
1508	6635	11822	1.14	8.1E-02	AB017138.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcI, and mdcM genes), complete cds
4831	10041	15180	0.68	8.1E-02	BF343921.1	EST_HUMAN	602015608F1 NCL_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4151640 5'
4831	10041	15181	0.68	8.1E-02	BF343921.1	EST_HUMAN	602015608F1 NCL_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4151640 5'
6	7681	10530	3.97	8.0E-02	AW554653.1	EST_HUMAN	EST3586723 MAGE resequences, MAGEC Homo sapiens cDNA
1713	7923	12042	8.38	8.0E-02	D26835.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1713	7923	12043	8.36	8.0E-02	D26835.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1909	7028	12248	3.28	8.0E-02	BE087219.1	EST_HUMAN	PM3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA
2448	7650		3.13	8.0E-02	BF246744.1	EST_HUMAN	60185548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075818 5'
2655	8019	13185	0.87	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome, segment 5/5
3794	8831	14079	0.73	8.0E-02	AW666118.1	EST_HUMAN	EST378191 MAGE resequences, MAGEC Homo sapiens cDNA
4046	8177		0.68	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
4743	8853	15004	1.19	8.0E-02	AK34202.1	EST_HUMAN	BS1902x1 NCL_CGAP_Qas4 Homo sapiens cDNA clone IMAGE:2132114 3'
4763	8856		6.97	8.0E-02	X72784.1	NT	M. musculus gene for gelatinase B
4898	10009	15154	0.65	8.0E-02	M28071.1	NT	Herpesvirus salivari transformation-associated protein (STP), and dihydrolipoamide succinyltransferase (DHFR) genes
2163	7266	12516	1.91	7.9E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959510 5'

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2949	8103	13268	8.92	7.9E-02	AI682029.1	EST_HUMAN	tr88408.x1 Barestad colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173648 3' similar to gp.226878
3928	8965	14116	4.62	7.8E-02	6881044	NT	60S RIBOSOMAL PROTEIN L38 (HUMAN);
3828	8865	14117	4.52	7.9E-02	6881044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4760	9893		1.37	7.8E-02	AB008018.1	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4884	9995	15141	1.78	7.8E-02	L24157.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
4892	10003		4.83	7.8E-02	AW081738.1	EST_HUMAN	Human bone sialoprotein (BSP) gene, exons 2, 3 and 4
1213	6345	11514	1.42	7.8E-02	AI763275.1	EST_HUMAN	x670a10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2881628 3'
1213	6345	11515	1.42	7.8E-02	AI763275.1	EST_HUMAN	cc58402.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1670487 5' similar to contains L1.13 L1
6071	8868		3.27	7.8E-02	BE250048.1	EST_HUMAN	repetitive element 1
1406	7917	11712	1.02	7.7E-02	AF181897.1	NT	repetitive element 1
3574	8716		1.89	7.7E-02	AJ288093.1	NT	600843055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859693 5'
3368	8513	13680	1.84	7.6E-02	BE514432.1	EST_HUMAN	Homo sapiens WRN (WRN) gene, complete cds
3389	8633	13694	0.89	7.6E-02	AA266447.1	EST_HUMAN	Homo sapiens period AF-4 gene, exons 2 to 7 and 3' and 3' repeat elements
785	6940	11088	1.54	7.5E-02	5902093	NT	601318428F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3834803 5'
785	5940	11089	1.54	7.5E-02	5902093	NT	EST112214 Corabedum II Homo sapiens cDNA 5' and similar to protocadherin 43
1824	7043	12263	1.21	7.5E-02	AL163278.2	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
477	5944	10765	1.44	7.4E-02	AW838547.1	EST_HUMAN	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
1473	6800		1.1	7.4E-02	AF030027.1	NT	Homo sapiens chromosome 21 segment HS21C078
2644	7947		1.03	7.4E-02	6755069	NT	RC5-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA
3580	8721	13879	1.02	7.4E-02	AI807885.1	EST_HUMAN	Equine herpesvirus 4 strain NS90367, complete genome
4872	8788	14933	1.11	7.4E-02	L78810.1	NT	Mus musculus pated-like homeodomain transcription factor 1 (Pitd1), mRNA
4763	9878	16027	2.6	7.4E-02	6978442	NT	wk43h01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2368386 3'
4919	10029	15171	1.6	7.4E-02	6878492	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
488	5638	10775	1.3	7.3E-02	BE984961.2	EST_HUMAN	Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA
488	5636	10778	1.3	7.3E-02	BE984961.2	EST_HUMAN	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchp1), mRNA
663	5841	10980	3.42	7.3E-02	AE001789.1	NT	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
1481	7819	11808	3.35	7.3E-02	AW800281.1	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
1866	7928		9.68	7.3E-02	AL163302.2	NT	Thermococcus maritima section 101 of 138 of the complete genome
4983	10081		1.11	7.3E-02	U12283.1	NT	CMO-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C102
							Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
116	5318	10460	0.97	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
118	5318	10461	0.97	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
1488	6813	11800	2.02	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1488	6813	11801	2.02	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2520	7824		1.57	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 28 reverse transcriptase (pol) gene, internal fragment, partial cds
3882	8938	14165	0.84	7.2E-02	AW288322.1	EST_HUMAN	UIH-BW70-ej-e-05-Q-UJ.e1 NCI CGAP Sub86 Homo sapiens cDNA clone IMAGE:2732049 3'
4323	9445	14578	5.25	7.2E-02	BF572307.1	EST_HUMAN	802077767F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251850 5'
1910	7028	12249	1.18	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2264	7374		1.21	7.1E-02	AE004890.1	NT	Pseudomonas aeruginosa PA01, section 451 of 628 of the complete genome
2268	7378	12828	4.24	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:4062081 5'
528	5892	10824	1	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1514	6841		1.12	7.0E-02	X98877.1	NT	Martellia Mibut-1 gene
3001	8168	13314	1.98	7.0E-02	AW138152.1	EST_HUMAN	UI-H-B11-ecy-c-07-Q-UJ.e1 NCI CGAP Sub83 Homo sapiens cDNA clone IMAGE:2716020 3'
3874	8010	14188	0.83	7.0E-02	AA815438.1	EST_HUMAN	al05at12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375878 3' similar to gb:K03002 60S
4018	9151	14283	1.09	7.0E-02	BE070284.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4111	9239		0.82	7.0E-02	AW782952.1	EST_HUMAN	QV4-BT0407-280100-090-s10 BT0407 Homo sapiens cDNA
4188	9314	14449	1.07	7.0E-02	AF077821.1	NT	CMO-UM0001-089300-270-e12 UM0001 Homo sapiens cDNA
4807	10017	15181	7.25	7.0E-02	BF381987.1	EST_HUMAN	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
512	5678	10810	12.18	6.9E-02	AL163210.2	NT	601818281F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:4050071 5'
512	5678	10811	12.18	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1338	8486		1.33	6.9E-02	4507888	NT	Homo sapiens chromosome 21 segment HS21C010
3770	8807	14050	1.06	6.9E-02	Q06394	SWISSPROT	Homo sapiens regulator of Gs-selective protein signalling (ZGAP1) mRNA, and translated products
3770	8907	14050	1.06	6.9E-02	Q06394	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
1912	7031	12251	2.82	6.8E-02	AF156973.1	NT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
3076	8228	13379	1.13	6.8E-02	AA781898.1	EST_HUMAN	Homo sapiens putative hepatic transcription factor (WBSR14) gene, complete cds
3076	8228	13380	1.13	6.8E-02	AA781898.1	EST_HUMAN	al75a08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376828 3'
3076	8228	13381	1.13	6.8E-02	AA781898.1	EST_HUMAN	al75a08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376828 3'
4528	9844		0.82	6.8E-02	BE141078.1	EST_HUMAN	al75a08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376828 3'
							MRO-HT0069-071089-001-c05 HT0069 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1543	8871		1.83	6.7E-02	AF115538.1	NT	Oncorhynchus mykiss TAP1 protein (OmyTAP1) mRNA, OmyTAP1T01 allele, complete cds
1800	7019	12239	1.1	6.7E-02	A1220285.1	EST_HUMAN	q978c04.x1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1841408 3'
3637	8835	13898	4.17	6.7E-02	P17278	SWISSPROT	HOMEOBOX PROTEIN HOXD3 (HOXA)
1355	8484	11684	2	6.8E-02	A1735503.1	EST_HUMAN	at12609.x1 Barcode aorta HPLR88 Homo sapiens cDNA clone IMAGE:2354920 3' similar to SW:LIN1_NYOCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.:
2163	7276	12523	1.53	6.8E-02	AJ289241.1	EST_HUMAN	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3445	8587	13750	8.96	6.8E-02	R64306.1	EST_HUMAN	y18b10.a1 Scores placenta N62HP Homo sapiens cDNA clone IMAGE:139579 3'
3459	8601	13765	2.65	6.8E-02		NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3459	8601	13768	2.66	6.8E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4057	9187	14329	1.66	6.8E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
4963	10071	15207	9.79	6.8E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
4963	10071	16208	9.79	6.8E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
580	5743	10871	1.6	6.8E-02	BF027639.1	EST_HUMAN	601871046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
888	6135	11305	2.02	6.8E-02	7706060	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1398	6526	11705	3.1	6.8E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1748	6874	12079	1.22	6.8E-02	AE000764.1	NT	Aquifex aeolicus section 96 of 109 of the complete genome
673	5737	10884	1.39	6.4E-02	X94549.1	NT	A. caeniense precursor of peridinin-chlorophyll-protein (PCP) gene
1748	6872	12076	1.04	6.4E-02	AE001777.1	NT	Thermidoga maritima section 89 of 136 of the complete genome
1748	6872	12077	1.04	6.4E-02	AE001777.1	NT	Thermidoga maritima section 89 of 136 of the complete genome
4871	8140	13304	1.09	6.4E-02	6896823	NT	Mus musculus histone deacetylase 5 (Hdac5), mRNA
1766	6882	12039	2.36	6.3E-02	AF109805.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; emRNP, G7A, NG23, MuiS homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
3989	8728		2.12	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
4228	8863	14486	4.28	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 68
4915	9437		1.88	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4556	8874		6.21	6.2E-02	Q62181	SWISSPROT	52 KD RO PROTEIN (SJOJGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO52)
253	5444	10568	3.71	6.1E-02	D16471.1	NT	Human mRNA, Xq terminal portion
3986	9101		2.78	6.1E-02	U73325.1	NT	Arabidopsis thaliana K ⁺ inward rectifying channel protein (AtKCI1) gene, complete cds
4624	9742	14884	0.98	6.1E-02	AF119413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACCS3) gene, complete cds
4624	9742	14885	0.98	6.1E-02	AF119413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACCS3) gene, complete cds
5152	10252	15391	28.79	6.1E-02	Y12503.1	NT	S. scrofa mRNA for Man9-mannosidase
1268	6395	11569	1.23	6.0E-02	AE001777.1	NT	Thermidoga maritima section 89 of 136 of the complete genome

Table 4

Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2637	7735	12089	1.12	8.0E-02	AW988948.1	EST_HUMAN	EST380924 MAGE resequences, MAGI Homo sapiens cDNA
2734	7828		1.27	8.0E-02	AB031289.1	NT	Mesocricetus crati mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2802	6302	10441	1.12	8.0E-02	AA188730.1	EST_HUMAN	2p76c04.r1 Stragatana HeLa cell c3 897216 Homo sapiens cDNA clone IMAGE:626310 5'
2802	6302	10442	1.12	8.0E-02	AA188730.1	EST_HUMAN	2p76c04.r1 Stragatana HeLa cell c3 897216 Homo sapiens cDNA clone IMAGE:626310 5'
3214	8385	13528	1.97	8.0E-02	AA372876.1	EST_HUMAN	EST84268 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3214	8385	13529	1.97	8.0E-02	AA372876.1	EST_HUMAN	EST84268 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
5081	10182	15318	4.4	8.0E-02	AF148738.1	NT	Rattus norvegicus testis specific protein mRNA, complete cds
228	5422	10559	4.39	5.0E-02	AW834718.1	EST_HUMAN	RC1-DT0001-280100-012-010 DT0001 Homo sapiens cDNA
2852	8108	13271	2.49	5.0E-02	AF160269.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
5106	10284	15403	0.87	5.0E-02	AW028748.1	EST_HUMAN	065388 F12F1.20 PROTEIN. ;
5108	10284	15404	0.87	5.0E-02	AW028748.1	EST_HUMAN	065388 F12F1.20 PROTEIN. ;
824	6802		4.76	5.0E-02	D80110.1	NT	Thiobacillus ferrooxidans marC, marA genes and URF-1
1673	6802	11997	1.12	5.0E-02	Q61768	SWISSPROT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
3640	8779	13934	1.86	5.0E-02	AE001776.1	NT	Thermoboga maritima section 87 of 138 of the complete genome
4332	9484	14589	4.08	5.0E-02	AW051927.1	EST_HUMAN	w24c02.x1 NCI CGAP K411 Homo sapiens cDNA clone IMAGE:2544578 3'
4332	9484	14580	4.08	5.0E-02	AW051927.1	EST_HUMAN	w24c02.x1 NCI CGAP K411 Homo sapiens cDNA clone IMAGE:2544578 3'
4620	8638	14784	5.07	5.0E-02	A1247505.1	EST_HUMAN	q1550101.X1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848897 3' similar to gbrM13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4620	8638	14785	5.07	5.0E-02	A1247505.1	EST_HUMAN	q1550101.X1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848897 3' similar to gbrM13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4546	8684		2.31	5.0E-02	AF086284.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
5165	10266	16394	0.63	5.0E-02	U76997.1	NT	Rattus norvegicus insulin-regulated membrane aminopeptidase IRAP mRNA, complete cds
5108	10269	15432	1.41	5.0E-02	S66288.1	NT	growth hormone [Syrian Golden hamsters, mRNA, 809 nt]
3029	8183	13338	1.34	5.7E-02	A1081644.1	EST_HUMAN	u63805.s1 NCI CGAP_B12 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
3043	8197	13353	1.42	5.7E-02	AF119117.1	NT	CE088111 ;
3685	8824		0.73	5.7E-02	AF001282.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3778	8916	14068	2.05	5.7E-02	AW986791.1	EST_HUMAN	Chironomus thummi thummi globin VIIA.1 (cgt-7A.1), globin 8.1 (cgt-8.1), globin II-beta (cgt-2beta), non-functional globin XIII (cgt-13RT), globin XII (cgt-12) and globin XI (cgt-11) genes, complete cds
1541	6669	11855	1.89	5.6E-02	AF094465.1	NT	EST378885 MAGE resequences, MAGI Homo sapiens cDNA
							Hydrocotyle rotundifolia ribosomal protein L16 (rpl16) gene, intron; chloroplast gene for chloroplast product

Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2266	7375		0.98	5.0E-02	BE904308.1	EST_HUMAN	601494578F2 NIH MGC_70 Homo sapiens cDNA clone IMAGE:3896610 5'
4610	9728	14864	1.2	5.0E-02	AB013100.1	NT	Lycopodium obscurum LE-ACS8 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4665	9781	14925	1	5.0E-02	AA280599.1	EST_HUMAN	z45c01.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3'
2616	7714	12987	3.87	5.0E-02	X97869.1	NT	H. sapiens gene encoding La autoantigen
3200	8351	13814	4.24	6.0E-02	6765501	NT	Mus musculus SH3 domain protein 1B (SH3d1B), mRNA
4190	8316	14450	1.05	5.0E-02	L41591.1	NT	Gallid herpesvirus mRNA fragment
1283	8422		2.32	8.4E-02	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
2891	8146		0.78	5.4E-02	AJ277483.1	NT	Oryza sativa rib5S-1 gene for putative Bowman Birk tyrosin inhibitor
3403	10315		8.25	8.4E-02	BE073469.1	EST_HUMAN	RC6-BT0659-140200-012-C03 BT0569 Homo sapiens cDNA
1065	8198	11360	1.75	6.3E-02	AW391248.1	EST_HUMAN	QV6-ST0213-021298-062-409 ST0213 Homo sapiens cDNA
1055	8198	11361	1.75	6.3E-02	AW391248.1	EST_HUMAN	QV6-ST0213-021298-062-409 ST0213 Homo sapiens cDNA
1521	6848	11836	3.37	5.3E-02	T84789.1	EST_HUMAN	yes37f12.1 Strategene lung (#637210) Homo sapiens cDNA clone IMAGE:119931 5' similar to gb:K01508
2488	7672	12825	1.3	5.3E-02	AJ276408.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
2808	8052	13233	0.7	6.3E-02	M59417.1	NT	Pseudomonas putida tgsS gene
2808	8052	13234	0.7	6.3E-02	M59417.1	NT	Drosophila melanogaster lamtlnh B2 gene, complete cds
3131	8282	13498	4.27	6.3E-02	AJ276408.1	NT	Drosophila melanogaster lamtlnh B2 gene, complete cds
5079	10174	15309	10.8	5.3E-02	M80463.1	NT	Pseudomonas putida tgsS gene
2281	7371		170.81	5.2E-02	5031808	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
3050	8243	13302	2.34	5.2E-02	AJ277681.1	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3090	8243	13393	2.34	5.2E-02	AJ277681.1	NT	Homo sapiens partial LMOT1 gene for LIM domain only 1 protein, exon 1
3912	8048	14207	0.7	5.2E-02	AF236101.1	NT	Homo sapiens partial LMOT1 gene for LIM domain only 1 protein, exon 1
4252	9371	14508	3.83	5.2E-02	U07192.1	NT	Arabidopsis thaliana putative dicarboxylate diiron protein (Grd1) mRNA, complete cds
2344	7451		0.99	5.1E-02	AL134071.1	EST_HUMAN	Human steroid hormone receptor Nr-1 mRNA, complete cds
4176	8302	14438	0.72	5.1E-02	AE001301.1	NT	DKFZp547D073.1 547 (synonym: Inr1) Homo sapiens cDNA clone DKFZp547D073 5'
482	6850	10788	1.14	5.0E-02	AF068004.1	NT	Chlamydia trachomatis section 28 of 87 of the complete genome
1207	6339	11508	14.64	5.0E-02	Z89104.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1891	7108	12341	2.34	5.0E-02	P02810	SWISSPROT	Bacillus subtilis complete genome (section 1 of 21); from 1 to 213080
2776	6134	11304	1.54	5.0E-02	U72742.1	NT	Salivary acidic proline-rich phosphoprotein 1/2 precursor (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-F/PIF-S) (PROTEIN A/PROTEIN C) [CONTAINS: PEPTIDE P-C]
3319	8466		1.4	5.0E-02	7305610	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3581	8722		0.87	5.0E-02	U32782.1	NT	Mus musculus Unc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3661	8800	13956	9.12	5.0E-02	U12769.2	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
						NT	Anthraxa pernyi perfolioblock protein homolog mRNA, complete cds

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
222	5415		32.46	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
367	5547	10580	3.03	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
367	5547	10691	3.03	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
2838	7893	13151	0.74	4.9E-02	U32636.1	NT	Zea mays phytoene synthase (Y1) gene, complete cds
3273	8422	13583	1.76	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (IDENTATORUBAL-PALLIDOLYSIAN ATROPHY PROTEIN)
3578	8719	13876	0.61	4.9E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
3678	8719	13877	0.61	4.9E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4808	9820	15061	5.76	4.9E-02	AW167821.1	EST_HUMAN	xq56g10.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2632388 3'
4808	9820	15062	6.76	4.9E-02	AW167821.1	EST_HUMAN	xq56g10.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2632388 3'
5178	10273		1.34	4.9E-02	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
328	5512	10850	1.16	4.9E-02	D18471.1	NT	Human mRNA, Xq terminal portion
329	5512	10850	2.96	4.9E-02	D18471.1	NT	Human mRNA, Xq terminal portion
468	5556	10763	0.88	4.9E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2252	7382	12818	1.13	4.9E-02	W51983.1	EST_HUMAN	z04802.s1 Soares_testis_fibroblasts_NHISF Homo sapiens cDNA clone IMAGE:325611 3' similar to
3193	8344	13508	1.77	4.9E-02	X17144.1	NT	gb:14303938 LUPUS KU AUTOANTIGEN PROTEIN P88 (HUMAN);
4842	9760		1.05	4.9E-02	Z54280.1	NT	Tetrahymena rostrata histone H4II and histone H4II intergenic DNA
5109	10210	16347	0.61	4.9E-02	U91914.1	NT	S. acrota gene for skeletal muscle ryanodine receptor
4896	10102	16233	0.63	4.7E-02	6881261	NT	Streptococcus constellatus D-alanine ligase gene, partial cds
268	5458	10598	2.47	4.6E-02	BE163583.1	EST_HUMAN	Rattus norvegicus Nestin (Nes), mRNA
738	5804	11046	2.37	4.6E-02	AED00445.1	NT	PMO-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA
				4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1685 section 335 of 400 of the complete genome
1298	6425		0.98	4.6E-02	AI014255.1	EST_HUMAN	am50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TRIP80533
1388	6498	11678	2.37	4.6E-02	AV727059.1	EST_HUMAN	P00533 LIMA; contains element LTR1 repetitive element;
				4.6E-02	AW236023.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HT0339
2482	7588	12819	1.62	4.6E-02	AW236023.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1;
2769	6498	10598	1.92	4.6E-02	BE163583.1	EST_HUMAN	PMO-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA
3477	8134	13287	0.82	4.6E-02	BE163583.1	EST_HUMAN	PMO-HT0339-251189-003-g05 HT0339 Homo sapiens cDNA
4896	9224		0.89	4.6E-02	AF220365.1	NT	Mus musculus nuclear RNA helicase II(Gu (d6c21) gene, complete cds
446	5514	10760	2.59	4.5E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1221	6353	11622	0.94	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1875/Ozolin VP35 gene, complete cds
1221	6353	11623	0.94	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1875/Ozolin VP35 gene, complete cds
1816	6339	12168	3.29	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2100	7215	12462	2.27	4.5E-02	AE003864.1	NT	Xylella fastidiosa, section 110 of 229 of the complete genome

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3703	8841	13998	4.15	4.9E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
217	5411		3.43	4.4E-02	BE972733.1	EST_HUMAN	801652164F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3933388 5'
1028	6167	11333	2.5	4.4E-02	L18289.1	NT	Drosophila melanogaster extracellular (EXO) mRNA, complete cds
2087	7203		1.94	4.4E-02	P31588	SWISSPROT	HYPOTHETICAL PROTEIN (ORF 2280)
2483	7667	12820	1.02	4.4E-02	AW1875475.1	EST_HUMAN	QV2-P10012-010300-070-Q02 PT0012 Homo sapiens cDNA
3818	8767	13913	1.99	4.4E-02	AF159180.1	NT	Mycobacterium xenopus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4598	9714	14860	1.03	4.4E-02	AF108907.1	NT	Homo sapiens S184 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4598	9714	14851	1.03	4.4E-02	AF108907.1	NT	Homo sapiens S184 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
781	5936	11094	6.58	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FMSA (FM3A) mRNA, complete cds
3411	8654	13713	8.38	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3638	8775		1	4.3E-02	AF090568.1	NT	Homo sapiens premysocytic leukemia zinc finger protein (PLZF) gene, complete cds
823	6378	11140	1.39	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
887	6018		1.81	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
897	6047	11218	0.73	4.2E-02	AW003645.1	EST_HUMAN	w634g01.X1 NCJ_CGAP_P11 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR-Q83281 Q83281 L1 RETROPOSON, ORF2 mRNA; contains L1.3 L1 L1 repetitive element;
1734	6891		2.38	4.2E-02	AL445086.1	NT	Thermoplasma acidophilum complete genome, segment 4/5
1788	6914	12121	1.13	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
3841	8780	13935	2.72	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4451	9570		7.38	4.1E-02	AW893484.1	EST_HUMAN	QV1-NM0012-180400-164-06 NM0012 Homo sapiens cDNA
3228	8378	13639	4.02	4.0E-02	AB040894.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3777	8914	14088	1.05	4.0E-02	L11910.1	NT	Human retinoblastoma susceptibility gene exon 1-21, complete cds
1121	6259	11424	2.98	3.9E-02	BF518149.1	EST_HUMAN	UHH-BW1-emo-h-09-Q-UJ.at1 NCJ_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1351	6480	11659	2.91	3.9E-02	P41047	SWISSPROT	PAS ANTIGEN LIGAND
1885	7082	12308	1.5	3.9E-02	AJ403383.1	NT	M.musculus DNA for desmin-binding fragment DesD7
2695	7781		1.76	3.9E-02	4606882	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kd (SDHC) mRNA
4110	8238	14376	1.12	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
4110	8238	14376	1.12	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5119	10220	16354	0.81	3.9E-02	AW592477.1	EST_HUMAN	RC8-ST0258-171189-021-C09 ST0258 Homo sapiens cDNA
5139	10230	16376	1.02	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5139	10230	16376	1.02	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
2110	7225		0.97	3.9E-02	AJ251973.1	NT	Homo sapiens partial eiserin-1 gene

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4908	10016	16180	0.88	3.8E-02	AU124122.1	EST_HUMAN	AU124122.NT2RM2 Homo sapiens cDNA clone NT2RM20071698 5'
983	6139	11309	4.31	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
2218	7330	12583	3.72	3.7E-02	A1984806.1	EST_HUMAN	wf85a08.x1 NC1 CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2494502 3'
3022	8176	13333	1.21	3.7E-02	P79044	SWISSPROT	ECMESODERMIN
3024	8178	13334	6.36	3.7E-02	BF312683.1	EST_HUMAN	601806233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5'
3436	8578		1.05	3.7E-02			Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kormu3), mRNA
3171	8322	13483	1.38	3.6E-02	AF000008.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 544001-777000 nt. position (3/7)
3631	8770	13928	0.77	3.6E-02	X73221.1	NT	H. vulgare Sa1 gene for sucrose synthase
3639	8778	13933	0.65	3.6E-02	AL096808.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10(10q26.3) of Homo sapiens
899	6046	11217	1.41	3.5E-02	U09508.1	NT	Drosophila melanogaster figgrin mRNA, complete cds
1009	6163	11320	1.03	3.5E-02	AF253417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1579	6708	11898	1.37	3.5E-02	BF678086.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1578	6708	11899	1.37	3.5E-02	BF678086.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4187	9313	14448	1.83	3.6E-02	AE001773.1	NT	Thermotoga maritima section 85 of 138 of the complete genome
4293	9416	14560	1.16	3.6E-02	P63780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
6177	10274		0.97	3.5E-02	P47144	SWISSPROT	HYPOTHETICAL 80.7 KD PROTEIN IN SOD1-GP2 INTERGENIC REGION
676	5740	10897	1.05	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
678	5740	10898	1.05	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
577	5740	10897	4.5	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
577	5740	10898	4.5	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1053	8184	11358	3.17	3.4E-02	AW274020.1	EST_HUMAN	x28d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814283 3' similar to SW: C211_HUMAN P63801 PUTATIVE SURFACE GLYCOPROTEIN C210RF1 PRECURSOR ;
1209	6341		8.4	3.4E-02	11348459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2389	7475	12720	1.38	3.4E-02	T57160.1	EST_HUMAN	yc28d06.r1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:81260 5' similar to contains MER29 repetitive element
3412	9555	13714	1.18	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008...
3766	8893	14043	0.85	3.4E-02	BE839514.1	EST_HUMAN	RC3-FN0165-060700-011-410 FN0165 Homo sapiens cDNA
3894	9030	14189	3.8	3.4E-02	AW784982.1	EST_HUMAN	RC3-UN0015-210200-021-A10 UN0015 Homo sapiens cDNA
4571	9689	14827	2.46	3.4E-02	X59789.1	NT	M. musculus S-antigen gene promoter region
5042	10144		2.26	3.4E-02	Q28457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5081	10163	15286	1.48	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
370	5550		21.46	3.3E-02	AA398735.1	EST_HUMAN	Z76508.61 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728188 3'
1169	6304	11470	9.4	3.3E-02	AB038867.1	NT	Cholesteryl esterase CYP2A17 mRNA for cytochrome P450 2A17, complete cds
1650	6778	11970	1.49	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2077	7193		1.25	3.3E-02	R09112.1	EST_HUMAN	Y25509.1 Soares fetal liver spleen INFL3 Homo sapiens cDNA clone IMAGE:127698 5'
2428	7632	12785	0.95	3.3E-02	6755882	NT	Mus musculus tumor rejection antigen gp98 (Tirat), mRNA
3342	8488	13654	1.18	3.3E-02	H02389.1	EST_HUMAN	Y55102.1 Soares placenta Nk2-IP Homo sapiens cDNA clone IMAGE:150771 5'
4148	8778	11970	2.58	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
4448	9568	14707	2.2	3.3E-02	6755882	NT	Mus musculus tumor rejection antigen gp98 (Tirat), mRNA
4778	9892	15039	0.63	3.3E-02	AW276698.1	EST_HUMAN	xp40504.x1 NC1_C3AP_HN11 Homo sapiens cDNA clone IMAGE:2742789 3'
127	6326	10471	1.73	3.2E-02	AJ002005.1	NT	Oryzobagus cuticulatus gene encoding leal sodium-dependent bile acid transporter
1127	6264	11428	15.01	3.2E-02	AF098275.1	NT	Drosophila melanogaster heat shock protein 88 (hsp88) gene, hsp88 allele, complete cds
1127	6264	11428	15.01	3.2E-02	AF098275.1	NT	Drosophila melanogaster heat shock protein 88 (hsp88) gene, hsp88 allele, complete cds
2108	7223		2.07	3.2E-02	P28955	SWISSPROT	LARGE TEGUMENT PROTEIN
2802	6326	10471	0.63	3.2E-02	AJ002005.1	NT	Oryzobagus cuticulatus gene encoding leal sodium-dependent bile acid transporter
3112	8265	13420	9.38	3.2E-02	BE887353.1	EST_HUMAN	601442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849727 5'
3893	8831	13998	1.21	3.2E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
3933	8069	14224	0.66	3.2E-02	Z74103.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL0550
3933	8069	14225	0.66	3.2E-02	Z74103.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL0550
4194	8319		14.19	3.2E-02	X04768.1	NT	H.sapiens RP3 gene (XLRP gene 3)
4793	9846	14992	3.38	3.2E-02	AF114182.1	NT	Saccharomyces cerevisiae (baker's yeast) gene encoding chloroplast protein, partial cds
4924	10034		1.54	3.2E-02	AF108906.1	NT	Mus musculus MHC class III region RD gene, partial cds; B1, C2, GBA, NG22, G9, HSP70, HSP70, HSC70, end emRNP genes, complete cds; G7A gene, partial cds; and unknown genes
1284	6593		2.27	3.1E-02	4503416	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1309	8439	11815	1.45	3.1E-02	P18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1878	7053		1.31	3.1E-02	Z50097.1	NT	Drosophila melanogaster mRNA for headcase protein
1835	8764		2.14	3.0E-02	AF187125.1	NT	Plyketines ribonucleoside cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
3582	8853	13855	1.07	3.0E-02	M94178.1	NT	Saccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds
3630	8769	13925	2.46	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3728	8853		0.82	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0288-150200-040-508 ST0288 Homo sapiens cDNA
3920	8066		1.08	3.0E-02	AA384003.1	EST_HUMAN	EST14530 Pituitary gland II Homo sapiens cDNA 5' end
4681	9777		12.98	3.0E-02	A1240487.1	EST_HUMAN	q10g08.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844314 3'
5032	10134	15264	6.82	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5032	10134	16266	8.82	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3546	8887	13850	0.77	2.9E-02	X65294.1	NT	Sheep gene for ultra high-sulphur keratin protein
3803	8039	14189	0.71	2.8E-02	H72805.1	EST_HUMAN	yu07e10.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:233130 5'
3958	8083	14245	1.34	2.8E-02	O15440	SWISSPROT	MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 5 (ABC TRANSPORTER MOAT-C) (PABG11)
584	5728		0.84	2.8E-02	AW970163.1	EST_HUMAN	EST382234 IMAGE resequencing, MAGK Homo sapiens cDNA
3349	8494	13861	1.12	2.8E-02	AF068063.1	NT	Homo sapiens retinal fasciclin (FSCN2) gene, exon 2
3349	8494	13862	1.12	2.8E-02	AF068063.1	NT	Homo sapiens retinal fasciclin (FSCN2) gene, exon 2
4289	8411		0.77	2.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV7S1P, TCRBV2S1A2N1T, TCRBV5S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
1499	6828	11813	1.13	2.7E-02	U69059.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 8
3413	8896	13716	1.71	2.7E-02	AL161494.2	NT	y98h12.r1 Soares multiple sclerosis_2NBH1MSP Homo sapiens cDNA clone IMAGE:280487 5'
4174	8300	14435	1.88	2.7E-02	N47258.1	EST_HUMAN	y98h12.r1 Soares multiple sclerosis_2NBH1MSP Homo sapiens cDNA clone IMAGE:280487 5'
4174	8300	14436	1.88	2.7E-02	N47258.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
570	5734	10882	0.94	2.6E-02	AL163282.2	NT	IL3-CT0219-280100-082-C08 CT0219 Homo sapiens cDNA
1377	6906		1.09	2.6E-02	AW850515.1	EST_HUMAN	ab02b02.a1 Strategene fetal retina 837202 Homo sapiens cDNA clone IMAGE:833958 3'
2348	7453	12708	1.83	2.6E-02	AA490021.1	EST_HUMAN	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2348	7455	12709	2.45	2.6E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2348	7455	12709	2.45	2.6E-02	6754241	NT	Mus musculus MHC class III region RD gene, partial cds; B7, C2, G9A, NG22, G9, HSP70, HSP70, HSC70, end smRNP genes, complete cds; G7A gene, partial cds; and unknown genes
2881	8035		1.28	2.6E-02	AF108008.1	NT	Chicken dorsalin-1 mRNA, complete cds
3837	8073		0.96	2.6E-02	AW181943.1	EST_HUMAN	x68f09.x1 Soares NFL_T_GBC ST Homo sapiens cDNA clone IMAGE:2862409 3'
4878	8989	15135	2.43	2.6E-02	L12032.1	NT	Dalmanella radiodurans R1 section 151 of 228 of the complete chromosome 1
5047	10149	15278	1.7	2.6E-02	AE002014.1	NT	Q15041 HYPOPHYSAL PROTEIN KIAA0068
5077	10178	16313	1.95	2.6E-02	AW241154.1	EST_HUMAN	ar28b06.y6 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
530	5698	10828	1.82	2.5E-02	AJ769130.1	EST_HUMAN	ar28b06.y6 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
530	5698	10829	1.82	2.5E-02	AJ769130.1	EST_HUMAN	ar28b06.y6 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
810	5963	11125	14.46	2.5E-02	BE974314.1	EST_HUMAN	60188030R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950885 3'
870	6021	11192	4.63	2.5E-02	BE974314.1	EST_HUMAN	60188030R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950885 3'
2724	7819		2.23	2.5E-02	U12571.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds
2923	8077	13245	3.22	2.5E-02	X89697.1	NT	H. carterae mRNA for fucoseanilin chlorophyll a/c binding protein, Fcp1

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2823	8077	13246	3.22	2.5E-02	X88897.1	NT	H. catenae mRNA for fucoxanthin chlorophyll <i>a/c</i> binding protein, Fcp1
4018	10308	14294	0.93	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4018	10308	14295	0.93	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4178	9304	14439	5.14	2.5E-02	AW592114.1	EST_HUMAN	h36h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA IMAGE:2834016 3'
5083	10312		11.72	2.5E-02	A1754201.1	EST_HUMAN	cr21111.x1 Jia bone marrow stroma Homo sapiens cDNA IMAGE:2834016 3'
189	6384	10503	0.53	2.4E-02	A178582.1	EST_HUMAN	cr21111.x1 Soares_NHIMPu_S1 Homo sapiens cDNA IMAGE:2070188 3'
1811	8739	11833	1.88	2.4E-02	H83894.1	EST_HUMAN	y75f11.l1 Soares fetal liver spleen 1NFS Homo sapiens cDNA IMAGE:211149 6'
2038	7831	12385	0.98	2.4E-02	P01801	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
2038	7831	12388	0.88	2.4E-02	P01801	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4347	9469	14808	1.59	2.4E-02	J05110.1	NT	T. thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
4405	9814	14764	1.33	2.4E-02	P01801	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4485	9814	14756	1.38	2.4E-02	P01801	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
5175	10272		1.2	2.4E-02	AF134513.1	NT	Kadipiro virus segment 6 VP6 gene, complete cds
1882	7002		2.4	2.3E-02	W05340.1	EST_HUMAN	z884g08.r1 Soares_fetal_lung_NbHL18W Homo sapiens cDNA IMAGE:288284 5'
1885	7014		3.49	2.3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2830	7437	12690	1.38	2.3E-02	Z74293.1	NT	S. cerevisiae chromosome IV reading frame ORF YOL245c
3659	8788	13954	5.18	2.3E-02	Z20377.1	EST_HUMAN	HSAACACADH.P, Human fetal Brain White tissue Homo sapiens cDNA
3694	8832		2.23	2.3E-02	L23429.1	NT	Canis beta-galactosidase-binding lectin (LGAL53) mRNA, 3' end
4121	9249	14383	0.69	2.3E-02	L24789.1	NT	Gallus gallus oomycin 45.8 (Cx45.8) gene, complete cds
4121	9249	14387	0.69	2.3E-02	L24789.1	NT	Gallus gallus oomycin 45.8 (Cx45.8) gene, complete cds
4388	9518	14859	1.03	2.3E-02	AW589107.1	EST_HUMAN	CM4-NN0080-280400-160-b04 NN0080 Homo sapiens cDNA
4427	8847	14886	0.9	2.3E-02	BE593226.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4427	8847	14887	0.9	2.3E-02	BE593226.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4428	10309	14888	0.75	2.3E-02	AW589383.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4428	10309	14889	0.75	2.3E-02	AW589383.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4667	8885	14824	2.62	2.3E-02	BF026487.1	EST_HUMAN	h36h08.x1 NCI_CGAP_U12 Homo sapiens cDNA IMAGE:2770871 3'
4667	8885	14825	2.62	2.3E-02	BF026487.1	EST_HUMAN	h36h08.x1 NCI_CGAP_U12 Homo sapiens cDNA IMAGE:2770871 3'
5132	10232	15387	0.78	2.3E-02	AF257110.1	NT	601672778F1 NIH_MGC_20 Homo sapiens cDNA IMAGE:3955388 5'
5132	10232	15388	0.78	2.3E-02	AF257110.1	NT	601672778F1 NIH_MGC_20 Homo sapiens cDNA IMAGE:3955388 5'
							Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
							Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
							Columbia livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
736	5892	11044	2.95	2.2E-02	AF018287.1	NT	complete cds
1769	6885		1.44	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
1772	6898	12105	1.12	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1772	6898	12108	1.12	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2011	7128	12365	1.12	2.2E-02	Z82001.1	NT	S.pneumoniae pcplA gene and open reading frames
3418	8558		1.84	2.2E-02	AA577785.1	EST_HUMAN	m24a04.01 NCI_CGAP_Gest1 Homo sapiens cDNA clone IMAGE:1084782 3'
3824	8763		4.07	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain ILA VP1 gene, complete cds
3832	8898	14122	1.16	2.2E-02	AW601317.1	EST_HUMAN	PMO-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA
3863	9026	14188	0.88	2.2E-02	Z74283.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
4535	9703		1.38	2.2E-02	P16789	SWISSPROT	HYPOTHETICAL PROTEIN UL21
5048	10150	15280	0.92	2.2E-02	Z73597.1	NT	S.cerevisiae chromosome XVI reading frame ORF YPL241c
5172	9028	14188	2.31	2.2E-02	Z74283.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
418	5386		4.02	2.1E-02	AV761602.1	EST_HUMAN	AV761602 MDS Homo sapiens cDNA clone MDSAD301 5'
448	5818		6.76	2.1E-02	AF028728.1	NT	Dicystatium discoideum histidine kinase C (dhkC) mRNA, complete cds
1267	6396	11570	6.19	2.1E-02	U72073.1	NT	Bacillus subtilis cdkLM cluster, Cdk (cdk), and spore coat protein CdkM (cdkM) genes, complete cds
1782	6918	12128	1.15	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1792	6918	12127	1.15	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1792	6918	12128	1.15	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
2777	5934	11092	3.07	2.1E-02	N29288.1	EST_HUMAN	YK4307.1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:284541 5'
3128	7146	12386	4.84	2.1E-02	BE072548.1	EST_HUMAN	PM2-BT0548-120100-001-f11 BT0548 Homo sapiens cDNA
3128	7146	12387	4.84	2.1E-02	BE072548.1	EST_HUMAN	PM2-BT0548-120100-001-f11 BT0548 Homo sapiens cDNA
3571	8712	13872	1.16	2.1E-02	AA461271.1	EST_HUMAN	z68509.1 Soares fetal_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786121 5'
4102	9231	14388	0.6	2.1E-02	Z74283.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
4286	9408	14644	0.7	2.1E-02	BF343655.1	EST_HUMAN	50201630661 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4161161 5'
4423	8543	14682	1.79	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds, and unknown genes
4433	9652	14696	1.33	2.1E-02	AI768127.1	EST_HUMAN	wg81411.x1 Soares_NSF_F8_9W_OT_PA_P_ST Homo sapiens cDNA clone IMAGE:23371608 3'
4472	9691		18.42	2.1E-02	Y19213.1	NT	Homo sapiens putative psilHbA pseudogene for hair keratin, exons 2 to 7
4849	9691		1.54	2.1E-02	Y19213.1	NT	Homo sapiens putative psilHbA pseudogene for hair keratin, exons 2 to 7
4877	9768	14839	4.85	2.1E-02	Y08501.1	NT	A.thaliana mitochondrial genome, part A
4898	9814	14982	0.72	2.1E-02	AA685737.1	EST_HUMAN	ag55g12.81 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126818 3'
4788	8901	15042	0.67	2.1E-02	AI822432.1	EST_HUMAN	wh54ed5.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3'
17	5228	10340	1.16	2.0E-02	BF002832.1	EST_HUMAN	7851608.x1 NCI_CGAP_P228 Homo sapiens cDNA clone IMAGE:3300998 3' similar to contains MER1.13
18	6229	10341	7.62	2.0E-02	AW895685.1	EST_HUMAN	MER1 repetitive element
258	5447	10585	2.69	2.0E-02	8753835	NT	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
283	5481	10623	2.38	2.0E-02	AA466538.1	EST_HUMAN	Mus musculus DmbB homolog 1 (E. coli) (Dmb1), mRNA
789	6863	11113	1.41	2.0E-02	8753835	NT	eat15b10.1 Soares_NHMPu_ST Homo sapiens cDNA clone IMAGE:813307 5'
							[Mus musculus DmbB homolog 1 (E. coli) (Dmb1), mRNA]

Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1088	6227	11382	1.21	2.0E-02	AL096805.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1(p36.33) of Homo sapiens
1202	6335	11505	1.33	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
1202	6335	11506	1.33	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
1883	7003	12221	1.29	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
1883	7003	12222	1.29	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
2768	7653		2.22	2.0E-02	AL161632.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3051	5228	10340	1.17	2.0E-02	BF002832.1	EST_HUMAN	7651608.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3308898 3' similar to contains MER1.53
3122	8274		1.44	2.0E-02	7305474	NT	MER1 repetitive element;
3212	8363		1.28	2.0E-02	AF095588.1	NT	Mus musculus serpin domain, transmembrane domain (TM), and cytoplasmic domain, (serpinophorin) 6B
3981	9115	14263	1.18	2.0E-02	M18095.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
6093	10183		2.7	2.0E-02	A1271895.1	EST_HUMAN	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
691	5848	10991	1.77	1.9E-02	AA672764.1	EST_HUMAN	q83c03.x1 NCI_CGAP_K03 Homo sapiens cDNA clone IMAGE:1888076 3'
1828	6767	11051	0.95	1.9E-02	P18488	SWISSPROT	rrf18a07.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:914186 similar to contains L1.11 L1
2033	7161	12391	1.63	1.9E-02	AL163303.2	NT	repetitive element;
2870	8024	13190	7.47	1.9E-02	AA719859.1	EST_HUMAN	EMPTY SPIRACLES HOMEOTIC PROTEIN
2919	8073	13243	1.57	1.9E-02	AV164659.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
3695	8734		1.05	1.9E-02	NS2250.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
3681	8820		9.11	1.9E-02	BE738088.1	EST_HUMAN	hw04905.s1 NCI_CGAP_S51 Homo sapiens cDNA clone IMAGE:1288337 3'
3695	8833	13987	0.72	1.9E-02	A1301183.1	EST_HUMAN	AV648689 GLC Homo sapiens cDNA clone GLCBLH07 3'
4021	9153	14297	1.39	1.9E-02	AF141940.1	NT	y228b02.s1 Soares_multiple_sclerosis_ZNF1MSP Homo sapiens cDNA clone IMAGE:284331 3'
4165	9291	14428	1.59	1.9E-02	P08081	SWISSPROT	601572882F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5'
4165	9291	14428	1.59	1.9E-02	P08081	SWISSPROT	qr04c07.x1 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1897280 3' similar to contains Alu repetitive element
4514	9832	14777	2.89	1.9E-02	A1452859.1	EST_HUMAN	Myoplasma imitans VHA1 precursor (VHA1) and VHA2 precursor (VHA2) genes, partial cds.
4698	7581	12832	2.69	1.9E-02	AL161650.2	NT	HOMEOTIC BICOID PROTEIN (PRD-4)
343	5628	10882	2.13	1.9E-02	AW771104.1	EST_HUMAN	HOMEOTIC BICOID PROTEIN (PRD-4)
1182	6297	11483	1.42	1.8E-02	X17694.1	NT	46804.x1 Soares_NSF_F8_QW_OT_PA_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element
							contains Alu repetitive element
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
							hr52c016.x1 NCI_CGAP_C017 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element
							MER29 repetitive element;
							H. francisci mRNA for myelin basic protein (MBP)

Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2840	7798	12981	1.28	1.8E-02	AE004544.1	NT	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
3185	8348		0.88	1.8E-02	AI805829.1	EST_HUMAN	h62d09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2080286 3'
4083	9194		1.06	1.8E-02	AA881448.1	EST_HUMAN	h42d04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406935 3'
4408	9628	14668	1.25	1.8E-02	AW936363.1	EST_HUMAN	QV4-DT0021-301289-071-b11 DT0021 Homo sapiens cDNA
807	6057	11228	1.22	1.7E-02	BE394889.1	EST_HUMAN	601310828F1 NIH_JGFC_44 Homo sapiens cDNA clone IMAGE:3832180 3'
1801	6926	12138	1.37	1.7E-02	AW573183.1	EST_HUMAN	h634d03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.11 L1 repetitive element
1801	6926	12139	1.37	1.7E-02	AW573183.1	EST_HUMAN	h634d03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.11 L1 repetitive element
1881	7001		1.44	1.7E-02	AL183204.2	NT	Homo sapiens chromosome 21 segment H921C004
2102	7217		5.4	1.7E-02	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin28, complete cds
2806	8120	13284	1	1.7E-02	AI147816.1	EST_HUMAN	q22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1690682 3'
3497	8638		4.28	1.7E-02	AW827388.1	EST_HUMAN	hm45a04.x1 NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element
4140	9288		1.01	1.7E-02	AA669818.1	EST_HUMAN	sc19f04.s1 Sirelagana ovary (#837217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element
4172	9288		2.34	1.7E-02	RO2505.1	EST_HUMAN	repetitive element contains element MER24 repetitive element
4432	9551	14694	0.82	1.7E-02	AI305278.1	EST_HUMAN	y686f08.r1 Soares_fetal_liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124947 5'
4602	9821	14783	1.68	1.7E-02	AW573183.1	EST_HUMAN	q108g07.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb:552359 ZINC FINGER PROTEIN 30 (HUMAN)
4692	8798	14943	2.08	1.7E-02	V00841.1	NT	h634d03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.11 L1 repetitive element
4782	8896		6.03	1.7E-02	AI016076.1	EST_HUMAN	l1messenger RNA for angiotensin (Lophius americanus) somatostatin II
5163	10263	15392	0.82	1.7E-02	AI251873.1	NT	ov61e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1840858 3'
510	5876		1.55	1.6E-02	AL021929.1	NT	Homo sapiens partial steerin-1 gene
1689	6798	11894	0.68	1.6E-02	Y18889.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 13/162
2230	7342	12596	1.45	1.6E-02	Q84176	SWISSPROT	Treponema mallophilum Tre2, Tre3 and Tre4 genes for flagellin subunit proteins and CAP protein homologues
2230	7342	12596	1.45	1.6E-02	Q84176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2606	7705	12081	1.4	1.6E-02	AA494872.1	EST_HUMAN	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2655	7763		1.13	1.6E-02	AB014534.1	NT	nc81d03.s1 NCI_CGAP_Ewt Homo sapiens cDNA clone IMAGE:3910867
2889	8144	13306	0.68	1.6E-02	AF11282.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
3512	8653	13819	4.35	1.6E-02	AW650652.1	EST_HUMAN	Laesaea sp. isolate 1bD cytochrome oxidase III gene, partial cds; mitochondrial gene for mitochondrial product IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3826	8952	14112	0.91	1.0E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
4148	9274		2.14	1.0E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIF61, Fas-binding protein, BING1, tapasin, RAGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Scam21 gene, partial>
4276	8389	14540	1.02	1.0E-02	AW876407.1	EST_HUMAN	QV2-PT0012-140100-030-007 PT0012 Homo sapiens cDNA
760	5908		33.34	1.0E-02	8923734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2127	7241	12483	1.83	1.0E-02	N39521.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
2164	7267	12816	1.33	1.0E-02	AL181594.2	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3033	8187	13342	1.72	1.0E-02	AJ008216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3033	8187	13343	1.72	1.0E-02	AJ008216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3705	8843	13908	0.9	1.0E-02	BF092942.1	EST_HUMAN	MIR4-TN0115-080900-201-b12 TN0115 Homo sapiens cDNA
416	5994		1.44	1.4E-02	AE002230.2	NT	Chlamydomonas reinhardtii R39, section 58 of 84 of the complete genome
1119	6257	11421	3.44	1.4E-02	7705680	NT	Homo sapiens NESH protein (LOC51225), mRNA
1280	6389		2.71	1.4E-02	U32600.1	NT	Haemophilus influenzae Rd section 116 of 163 of the complete genome
1302	6432		2.7	1.4E-02	U87779.1	NT	Xenopus laevis neurogranin related 1b (X-NGNR-1b) mRNA, complete cds
1403	6531		2.39	1.4E-02	AF216854.1	NT	Homo sapiens headlup gene, complete cds
1532	6659		0.97	1.4E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBAHH11 5'
3197	8348	13510	2.4	1.4E-02	AF160889.2	NT	Bifidobacterium longum Nav+/+ antipeptide (nha3), cytosolic deaminase, and alpha-glucosidase (agtl.) genes, complete cds; and N-acetylglucosaminylase repressor protein (nagCkyR) gene, partial cds
3379	8624	13687	0.87	1.4E-02	AW074212.1	EST_HUMAN	Xb080f09.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575783 3'
3466	8608	13772	6.96	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3466	8608	13773	5.95	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3505	8946	13812	1.17	1.4E-02	4503628	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3633	8772	13928	7.72	1.4E-02	6988918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-B), mRNA
4466	8585	14723	6.9	1.4E-02	AW962888.1	EST_HUMAN	Mus musculus histocompatibility 2, complement component factor B (H2-B), mRNA
4466	8585	14724	6.9	1.4E-02	AW962888.1	EST_HUMAN	EST374761 IMAGE resequences, MAGG Homo sapiens cDNA
4847	8959	15102	8.95	1.4E-02	BE733142.1	EST_HUMAN	EST374761 IMAGE resequences, MAGG Homo sapiens cDNA
4847	8959	15103	8.95	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_JMGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
1876	6396		0.98	1.3E-02	BE739263.1	EST_HUMAN	601567403F1 NIH_JMGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
1859	7076	12299	1.32	1.3E-02	AL163201.2	NT	601567403F1 NIH_JMGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
3198	8349	13511	1.97	1.3E-02	BF697081.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001
3198	8349	13512	1.97	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_JMGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3942	9078		1.27	1.3E-02	AF169288.1	NT	602129475F1 NIH_JMGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
						NT	Mus musculus beta-sarcoglycan gene, complete cds

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
210	5404		0.71	1.2E-02	X87344.1	NT	H. sapiens DIMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQ82 and RING8, 9, 13 and 14 genes
352	5334	10673	3.3	1.2E-02	AA059288.1	EST_HUMAN	286901.r1 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element:
452	5620	10763	2.68	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR6 REGION
737	5893	11045	0.77	1.2E-02	AI183522.1	EST_HUMAN	q688a12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.1 L1 repetitive element:
2157	7270	12818	1.14	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2160	7273	12521	1.21	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
2420	7625	12778	0.87	1.2E-02	AW172360.1	EST_HUMAN	X47609.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2457	7591	12813	1.27	1.2E-02	AL163216.2	NT	Homo sapiens chromosome 21 segment HS21C018
3076	8229		6.89	1.2E-02	AA075418.1	EST_HUMAN	zn88a03.r1 Strabagene ovarian cancer (#837219) Homo sapiens cDNA clone IMAGE:846020 5'
3272	8421	13582	1.85	1.2E-02	RG2805.1	EST_HUMAN	Y11608.s1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:138903 3'
4852	8994	15109	0.89	1.2E-02	6754367	NT	Mus musculus interferon regulatory factor 5 (Irif5), mRNA
4893	10004	15148	1.99	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5024	10126		1.27	1.2E-02	AB019788.1	NT	Cynops pyrogastrer Oplubiqf mRNA, partial cds
5088	10170	15305	1.77	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
1273	8402	11578	1.05	1.1E-02	AA070364.1	EST_HUMAN	zn68a1.1.s1 Strabagene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:530924 3'
1721	6848	12032	1.35	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
1721	6848	12053	1.35	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
2032	7160	12389	2.69	1.1E-02	BF345263.1	EST_HUMAN	6C2018037F1 NCI CGAP Bm87 Homo sapiens cDNA clone IMAGE:4153908 5'
2843	7898		3.8	1.1E-02	N89529.1	EST_HUMAN	zn40a05.t1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:285040 5'
3609	8650	13817	2.28	1.1E-02	AI653508.1	EST_HUMAN	tg95b10.x1 NCI CGAP OY28 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XPX_HUMAN
4082	8211		0.64	1.1E-02	AW813788.1	EST_HUMAN	Q92888 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL;
4788	8911	15032	2.21	1.1E-02	AL048383.2	EST_HUMAN	RC3-S10167-120200-018-g11 ST0187 Homo sapiens cDNA
6	5217	10331	7.57	1.0E-02	AW846120.1	EST_HUMAN	DKFZp586E0924.s1 688 (synonym: hube1) Homo sapiens cDNA clone DKFZp586E0924
3062	8216	13369	2.62	1.0E-02	BE835556.1	EST_HUMAN	MR9-CT0178-111089-003-e10 CT0178 Homo sapiens cDNA
3245	8395	13557	1.16	1.0E-02	BE968899.1	EST_HUMAN	RC0-FV0025-250500-021-402 FN0025 Homo sapiens cDNA
3493	8634		0.64	1.0E-02	AW845621.1	EST_HUMAN	601849987R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'
3559	8996	14162	0.78	1.0E-02	AI065086.1	EST_HUMAN	MR0-CT0060-081089-003-H10 CT0060 Homo sapiens cDNA
4744	9857	15005	4.26	1.0E-02	6753521	NT	HA0821 Human fetal liver cDNA library Homo sapiens cDNA
							Mus musculus corticotroph releasing hormone receptor 2 (Chr2), mRNA

Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4813	6825	15066	5.66	1.0E-02	R96567.1	EST_HUMAN	yq54h01.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:186633 6'
894	6044	11216	3.28	9.0E-03	A1766126.1	EST_HUMAN	wt4209.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
1268	6397		1.47	9.0E-03	BE781889.1	EST_HUMAN	MER22 MER22 repetitive element
1460	6818	11807	1.58	9.0E-03	AE001270.1	NT	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'
2372	7478	12732	1.4	9.0E-03	AL161598.2	NT	Trepurone pallidum section 86 of 87 of the complete genome
2871	8025	13191	0.8	9.0E-03	A1251744.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
2871	8025	13192	0.8	9.0E-03	A1251744.1	EST_HUMAN	q180f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3845	8784	13938	0.82	9.0E-03	J05184.1	NT	q180f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
4972	10080	15217	1.14	9.0E-03	BE047849.1	EST_HUMAN	S.acidocaldarius thermoplasma gene, complete cds
501	5666		2.57	9.0E-03	AA723007.1	EST_HUMAN	z44610.y1 NCL_CGAP_Brn62 Homo sapiens cDNA clone IMAGE:2281468 5'
890	6137	11306	83.35	8.0E-03	AF106656.1	NT	z44610.y1 NCL_CGAP_Brn62 Homo sapiens cDNA clone IMAGE:2281468 5'
2140	7254	12500	1	8.0E-03	AL163263.2	NT	z44610.y1 NCL_CGAP_Brn62 Homo sapiens cDNA clone IMAGE:2281468 5'
2928	8082		0.97	8.0E-03	U47048.1	NT	Alu repetitive element
3340	8486	13652	0.8	8.0E-03	AJ131016.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
3663	8752	13947	1.28	8.0E-03	P32844	SWISSPROT	Homo sapiens chromosome 21 segment HS21C083
3663	8752	13948	1.28	8.0E-03	P32844	SWISSPROT	Escherichia coli microcin 24 region, DNA binding protein (mcbA), immunity protein (mtf), microcin 24 (mtS).
4362	9484	14625	4.21	8.0E-03	BF363327.1	EST_HUMAN	and microcin transport protein (mtfA, mtfB) genes, complete cds
6164	10264	16363	0.84	8.0E-03	U02970.1	NT	Homo sapiens SCL gene locus
692	5849	10982	12.77	7.0E-03	AF097183.1	NT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
692	5849	10983	12.77	7.0E-03	AF097183.1	NT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
878	6124	11284	5.37	7.0E-03	AF243376.1	NT	GM4-NN0119-300600-223-505 NN0119 Homo sapiens cDNA
1117	6255	11419	2.78	7.0E-03	AV731712.1	EST_HUMAN	Protheca wickerhamii 263-11 complete mitochondrial DNA
1373	6601		1.02	7.0E-03	Q81060	SWISSPROT	Cryptosporidium parvum HC-10 gene, complete cds
1402	6630	11709	8.16	7.0E-03	AA688288.1	EST_HUMAN	Cryptosporidium parvum HC-10 gene, complete cds
1517	6844	11830	2.52	7.0E-03	AW303588.1	EST_HUMAN	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1763	6878	12084	1.23	7.0E-03	AW650556.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1763	6878	12085	1.23	7.0E-03	AW650556.1	EST_HUMAN	FORKHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE
2238	7836	12608	1.36	7.0E-03	PO4929	SWISSPROT	NUCLEAR FACTOR 3 FORK-HEAD HOMOLOG 2 (HNFH-2)
3544	8885	13847	0.73	7.0E-03	AJ150273.1	EST_HUMAN	ab79509.s1 Stratiogene field rethra 937202 Homo sapiens cDNA clone IMAGE:353145 3'
3747	8886	14036	0.72	7.0E-03	AW444463.1	EST_HUMAN	ab79509.s1 Stratiogene field rethra 937202 Homo sapiens cDNA clone IMAGE:2813739 3'

Table 4
Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3789	8928	14078	0.88	7.0E-03	AF190344.1	NT	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4572	9630		1.42	7.0E-03	AW630888.1	EST_HUMAN	H98a05.y1 NCJ_CGAP_GUT Homo sapiens cDNA clone IMAGE:2868686 5'
4674	10082		2.18	7.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5086	10186	15324	1.02	7.0E-03	BE044191.1	EST_HUMAN	h39h08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3039807 3' similar to TR:083434
5088	10186	15325	1.02	7.0E-03	BE044191.1	EST_HUMAN	h39h08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3039807 3' similar to TR:083434
1244	6376	11560	9.29	8.0E-03	AW611148.1	EST_HUMAN	h22a05.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXR_HUMAN O76469 ORPHAN NUCLEAR RECEPTOR PXR;
1244	6376	11551	9.29	8.0E-03	AW611148.1	EST_HUMAN	h22a05.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to SW:PXR_HUMAN O76469 ORPHAN NUCLEAR RECEPTOR PXR;
2857	8012	13174	1.7	8.0E-03	AA759135.1	EST_HUMAN	h78e11.s1 Scores_testis_NHT Homo sapiens cDNA clone 1321772 3'
2857	8012	13175	1.7	8.0E-03	AA759135.1	EST_HUMAN	h78e11.s1 Scores_testis_NHT Homo sapiens cDNA clone 1321772 3'
3229	8379		2.39	8.0E-03	H75680.1	EST_HUMAN	y77h04.t1 Scores_fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:211951 5'
3288	8435		1.13	8.0E-03	AF190338.1	NT	Neotoma sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3363	8508	13875	1.21	8.0E-03	U80880.1	NT	Fugu rubripes zinc finger protein, isotacin, fatty acid binding protein, sepiapterin reductase and vasotodin genes, complete cds
3363	8508	13876	1.21	8.0E-03	U80880.1	NT	Fugu rubripes zinc finger protein, isotacin, fatty acid binding protein, sepiapterin reductase and vasotodin genes, complete cds
3533	8975		1.12	8.0E-03	W37085.1	EST_HUMAN	zot3a11.t1 Scores_papillary tumor_NHHPA Homo sapiens cDNA clone IMAGE:322172 5'
3637	8776	13931	4.08	8.0E-03	BF510988.1	EST_HUMAN	UIHBJ4-epm-c-08-0-UI s1 NCJ_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3671	8810	13968	0.92	8.0E-03	BE077583.1	EST_HUMAN	RC1-BT0809-260400-014-407 BT0608 Homo sapiens cDNA
3768	8895	14046	1.2	8.0E-03	6754028	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnpl), mRNA
3886	9032	14192	1.21	8.0E-03	AW847284.1	EST_HUMAN	RCO-CT0204-240889-021-510 CT0204 Homo sapiens cDNA
3929	9086		0.8	8.0E-03	BE250108.1	EST_HUMAN	600942804F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2868613 5'
4342	9484		2.01	8.0E-03	AJ016833.1	EST_HUMAN	ov35c11.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4664	9780	14924	8.05	8.0E-03	AA324242.1	EST_HUMAN	EST27118 Carabellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
668	5828	10887	1.88	8.0E-03	U25105.1	NT	Chlamydia trachomatis partial ORF8; aminocacyl-ATP synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
668	5828	10888	1.88	8.0E-03	U25105.1	NT	Chlamydia trachomatis partial ORF8; aminocacyl-ATP synthase, complete cds; complete ORFA, and grpE-like protein, complete cds

Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
689	5828	10987	2.65	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthetase, complete cds; complete ORFA, and grpE-like protein, complete cds
689	5828	10988	2.65	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthetase, complete cds; complete ORFA, and grpE-like protein, complete cds
1113	6251	11415	0.99	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase RH9
2842	7740	12993	1.64	5.0E-03	AB033008.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2801	6066	13224	0.76	5.0E-03	BE265057.1	EST_HUMAN	6011B4789F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538769 5'
3114	8287	13423	3.72	5.0E-03	T87623.1	EST_HUMAN	yc81f09.s1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:22395 3'
3133	8284		2.08	5.0E-03	AL161481.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3145	8288	13455	1.14	5.0E-03	R71784.1	EST_HUMAN	y88g02.s1 Soares breast 2NHBst Homo sapiens cDNA clone IMAGE:155668 3'
3261	8410		0.99	5.0E-03	AJ287357.1	NT	Homo sapiens partial LIMD1 gene for LIM domain containing protein 1 and KIAA0851 gene
3876	8816	13971	3.63	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (pbpB) gene, complete cds
3739	8877	14028	0.7	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
3944	9080		1.49	5.0E-03	AA286075.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4261	9404	14543	0.65	5.0E-03	H78355.1	EST_HUMAN	y479g10.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:240068 5'
4283	8877	14028	0.77	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4580	9698	14835	1.3	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
4687	9803	14950	1.53	5.0E-03	AJ752897.1	EST_HUMAN	cm15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cm15c02 random
231	5423	10963	8.19	4.0E-03	AW500198.1	EST_HUMAN	UHFBNO-dic-h-04-0-ULr1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5'
319	5505	10843	1.71	4.0E-03	R49482.1	EST_HUMAN	y51e04.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:35988 3'
442	5910	10756	0.82	4.0E-03	P64675	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)
601	5763	10881	4.31	4.0E-03	AA030639.1	EST_HUMAN	cn75g12.s1 Soares NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1662568 3'
876	6028	11201	1.76	4.0E-03	R49482.1	EST_HUMAN	y51e04.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:35988 3'
912	6082		3.34	4.0E-03	AW749101.1	EST_HUMAN	RC3-BT0333-110100-012-101 BT0333 Homo sapiens cDNA
1152	6288	11453	23.83	4.0E-03	AA069777.1	EST_HUMAN	RC3-BT0333-110100-012-101 BT0333 Homo sapiens cDNA clone IMAGE:510568 5'
1171	6306	11473	1.43	4.0E-03	AW794740.1	EST_HUMAN	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1307	6437	11612	1.15	4.0E-03	AA284374.1	EST_HUMAN	z559a01.t1 NCI CGAP_G081 Homo sapiens cDNA clone IMAGE:701736 5'
1669	6727		1.29	4.0E-03	AV708305.1	EST_HUMAN	AV708305 ADC Homo sapiens cDNA clone ADCAK806 5'
1765	6881	12087	2.25	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and efferactory-fimbria associated protein AT1-48 mRNA, complete cds
2013	7130	12388	5.61	4.0E-03	AA059777.1	EST_HUMAN	z61a08.l1 Striatogen colon (R537204) Homo sapiens cDNA clone IMAGE:510598 5'
2228	7340		1.6	4.0E-03	BE410568.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2265	7365	12621	1.19	4.0E-03	AW794740.1	EST_HUMAN	RC8-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2537	7640	12888	1.09	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2637	7640	12889	1.09	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2682	7760	12889	2.57	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2682	7760	13000	2.57	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2687	7764	13003	1.11	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21 C084
3210	8367	13523	1.16	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151289-003-H08 HT0340 Homo sapiens cDNA
3210	8361	13524	1.16	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151289-003-H08 HT0340 Homo sapiens cDNA
3617	8668	13824	0.74	4.0E-03	AW188428.1	EST_HUMAN	X9304.X1 NCL CGAP_Co18 Homo sapiens cDNA clone IMAGE:2685279 3'
3617	8663	13825	0.74	4.0E-03	AW188428.1	EST_HUMAN	X9304.X1 NCL CGAP_Co18 Homo sapiens cDNA clone IMAGE:2685279 3'
3970	9104		1.84	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exon 1-11 (and joined CDS)
5187	10284		1.18	4.0E-03	C98921	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 6)
369	6549	10883	2.01	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
880	6030	11202	11.35	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1674	6903	11698	3.31	3.0E-03	AA468110.1	EST_HUMAN	nc79cd5.at NCL CGAP_P12 Homo sapiens cDNA clone IMAGE:782884 similar to contains Alu repetitive element
2270	7380		4.86	3.0E-03	Z32621.1	NT	S. cereale (cv. Halo) mRNA for triosephosphate isomerase
2681	8115		1.75	3.0E-03	Y09006.1	NT	Arabidopsis thaliana rpoM1 gene
3055	8208	13383	4.44	3.0E-03	BE376296.1	EST_HUMAN	60123782F NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608893 5'
3130	8281	13437	2.82	3.0E-03	AW802887.1	EST_HUMAN	IL2-UM0076-240300-058-D03 UM0076 Homo sapiens cDNA
3399	8543	13702	1.58	3.0E-03	U94806.1	NT	Mus musculus alpha-1(XVII) collagen (COL1A1) gene, exon 1 and 2
3408	8551		7.13	3.0E-03	Y12500.1	NT	C. elegans samde gene
3950	9085	14239	5.93	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 6'
3960	9085	14240	5.89	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 6'
4011	9144	14284	1.37	3.0E-03	AJ762278.1	EST_HUMAN	h10409.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1165688 5'
4122	9250		1.24	3.0E-03	Z32621.1	NT	S. cereale (cv. Halo) mRNA for triosephosphate isomerase
4374	9495	14639	13.02	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4482	9611	14751	4.99	3.0E-03	AJ580141.1	EST_HUMAN	h08.F10.H3 conorm Homo sapiens cDNA 3'
4801	9914	15055	3.48	3.0E-03	AJ732754.1	EST_HUMAN	h018a08.x3 Stratagene lung (h637210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element
4823	9935	15076	7.71	3.0E-03	BE787845.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'

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Table 4

Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5123	10224	15339	1	3.0E-03	4506414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5123	10224	15360	1	3.0E-03	4506414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5159	10259	15398	0.92	3.0E-03	S52213.1	NT	CD11b-leukocyte integrin alpha chain [human, Genomic, 104 nt, segment 23 of 31]
5174	10271	15412	1.32	3.0E-03	AW237754.1	EST_HUMAN	nm81c09.x1 NC1 CGAP_Ki671 Homo sapiens cDNA clone IMAGE:2680603 3'
513	5679	10812	0.77	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
513	5679	10813	0.77	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
788	7801		10.76	2.0E-03	T70874.1	EST_HUMAN	y415h03.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:108341 5'
1372	8500	11683	2.08	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1376	8503	11685	1.9	2.0E-03	AA061605.1	EST_HUMAN	nt68101.at1 NC1 CGAP_AVI1 Homo sapiens cDNA clone IMAGE:1217583
1384	8512	11683	5.44	2.0E-03	AF284448.1	NT	Homo sapiens tumor-related protein DRG2 (DRG2) gene, complete cds
1600	6827	11814	1.55	2.0E-03	P48509	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1631	6858	11844	1.76	2.0E-03	4557838	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1631	6858	11845	1.76	2.0E-03	4557838	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1604	6732		5.07	2.0E-03	P28400	SWISSPROT	COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR
1781	6907	12116	1.08	2.0E-03	AA450138.1	EST_HUMAN	z42a10.r1 Soares fetal testis Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:789114 5'
1898	7113	12348	1.27	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2543	7846		4.07	2.0E-03	AW137762.1	EST_HUMAN	UHH-B11-adi-g-10-Q-UI.at1 NC1 CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3398	8542	13701	3.39	2.0E-03	AA450138.1	EST_HUMAN	z42a10.r1 Soares fetal testis Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:789114 5'
3404	8547	13706	0.98	2.0E-03	BF668553.1	EST_HUMAN	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3843	8782	13936	5.48	2.0E-03	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
4089	9217	14353	1.66	2.0E-03	P03374	SWISSPROT	ENV POLYPEPTIDE [CONTAINS: GOAT PROTEIN GP52; GOAT PROTEIN GP36]
4197	9322		9.07	2.0E-03	U69491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4405	9328		0.96	2.0E-03	AW297380.1	EST_HUMAN	UHH-B1W0-adi-g-03-Q-UI.at1 NC1 CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730413 3'
4519	9637	14782	2.13	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4519	9637	14783	2.13	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4578	8794		1.47	2.0E-03	R87778.1	EST_HUMAN	y415e02.at1 Soares adult brain Nb2Hf8B65Y Homo sapiens cDNA clone IMAGE:180890 3'
5005	10110	16239	0.74	2.0E-03	AF003523.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5013	10116	16248	1	2.0E-03	D38157.1	NT	Equine rotavirus RNA 5 for NSP1, complete cds, strain: H2
5013	10116	15249	1	2.0E-03	D38157.1	NT	Equine rotavirus RNA 6 for NSP1, complete cds, strain: H2

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
438	6607	10761	1.54	1.0E-03	H96471.1	EST_HUMAN	y88c08.r1 Soares_joined_gland_N3H-PG Homo sapiens cDNA clone IMAGE:232834 5'
830	6982	11160	1.37	1.0E-03	A1720283.1	EST_HUMAN	as70b08.x1 Barstead codon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TRQ13825 Q13825 AU-BINDING PROTEINENOL-COA HYDRATASE ;
830	6982	11161	1.37	1.0E-03	A1720283.1	EST_HUMAN	as70b08.x1 Barstead codon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TRQ13825 Q13825 AU-BINDING PROTEINENOL-COA HYDRATASE ;
1096	6234	11397	3.44	1.0E-03	A1865788.1	EST_HUMAN	w465a08.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3'
1116	6254	11418	2.36	1.0E-03	A1954572.1	EST_HUMAN	w465a08.x1 NCL_CGAP_Mer15 Homo sapiens cDNA clone IMAGE:2651242 3'
1168	6303	11469	1.32	1.0E-03	A1692816.1	EST_HUMAN	w465a08.x1 NCL_CGAP_Ju24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to cortilins Alu repetitive element
2021	7138	12378	2.71	1.0E-03	P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMMI)
2137	7291	12497	1.97	1.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
2860	8104	13269	1.23	1.0E-03	AB033117.1	NT	Homo sapiens mRNA for KIAA1281 protein, partial cds
3174	8325	13488	2.13	1.0E-03	P18916	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3174	8325	13487	2.13	1.0E-03	P18916	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3284	8433	13696	0.8	1.0E-03	P08647	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3530	8672	13837	0.8	1.0E-03	U68061.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3530	8672	13838	0.8	1.0E-03	U68061.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3642	8761		1.48	1.0E-03	AB044400.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3688	9034	14193	1.14	1.0E-03	AW170562.1	EST_HUMAN	Human MUC2 gene, promoter region
3907	9043	14203	0.65	1.0E-03	Z49849.1	NT	Human MUC2 gene, promoter region
4412	8932	14971	2.51	1.0E-03	BE939162.1	EST_HUMAN	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15 contains TAR1.11 TAR1 repetitive element ;
4455	8574	14713	3.99	1.0E-03	BE248538.1	EST_HUMAN	S. cerevisiae chromosome X reading frame ORF YJ149w
4633	8761	14898	0.8	1.0E-03	U29449.1	NT	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
4792	8905	15045	2.14	1.0E-03	A1073485.1	EST_HUMAN	TCBAP1D4909 Pediatric pro-B cell acute lymphoblastic leukemia Baylar-HGSC project=TCBA Hemo sapiens cDNA clone TCBAP4909
4792	8905	15046	2.14	1.0E-03	A1073485.1	EST_HUMAN	Caenorhabditis elegans apical leader RNA (SL3 alpha), (SL4), and (SL5) genes
4793	8906		5.98	1.0E-03	BE154087.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
5060	10162	15295	10.91	1.0E-03	O46409	SWISSPROT	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
5195	10293	15430	2.16	1.0E-03	AW297269.1	EST_HUMAN	PMO-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
1498	6625		1.19	8.0E-04	X86468.1	NT	APOLIPROTEIN A-IV PRECURSOR (APO-AIV)
4161	9277		6.04	8.0E-04	P08547	SWISSPROT	UIH-BW0-ef-d-08-Q-U1.1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731838 3'
							X laevis mRNA for CASR protein
							LINE-1 REVERSE TRANSCRIPTASE HOMOLOG

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4730	8843	14989	2.53	8.0E-04	U28185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1841	6982	12185	1.08	7.0E-04	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2376	7482	12736	1.02	7.0E-04	U28185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2875	7772	13023	3.11	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3284	8413	13575	0.97	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
3831	9087	14223	1.49	8.0E-04	AI862525.1	EST_HUMAN	MJ15a11.x1 NCI_CGAP_K1412 Homo sapiens cDNA clone IMAGE2402878 3'
4190	9282	14418	3.13	8.0E-04	U45983.1	NT	Homo sapiens COR8 chemokine receptor (CMK8R8) gene, complete cds
4421	9541	14880	0.9	8.0E-04	BE179435.1	EST_HUMAN	RC2-HT0560-190200-011-09 HT0560 Homo sapiens cDNA
4421	9541	14881	0.9	8.0E-04	BE179435.1	EST_HUMAN	RC2-HT0560-190200-011-09 HT0560 Homo sapiens cDNA
5003	10108	15415	1.07	8.0E-04	L40808.1	NT	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5180	10277	15415	1.88	8.0E-04	BE089226.1	EST_HUMAN	CM2-BT0698-230300-128-F10 BT0698 Homo sapiens cDNA
650	5811	10948	9.89	5.0E-04	O10341	SWISSPROT	HYPOTHETICAL 29.3 KD PROTEIN (ORF82)
1616	6843		1.17	8.0E-04	AW851844.1	EST_HUMAN	QV6-CT0225-021050-030-07 CT0225 Homo sapiens cDNA
3396	8439	13698	1.31	6.0E-04	AA549331.1	EST_HUMAN	M27e11.s1 NCI_CGAP_C011 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element
390	5559		0.94	4.0E-04	BF241482.1	EST_HUMAN	601876534F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104897 5'
672	5631	10971	1.09	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 83 of 163 of the complete genome
848	5959	11170	1.25	4.0E-04	AI720283.1	EST_HUMAN	as70b08.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;
848	5959	11171	1.25	4.0E-04	AI720283.1	EST_HUMAN	as70b08.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825 Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;
1477	6804	11790	2.44	4.0E-04	AW753393.1	EST_HUMAN	RC3-CT0254-130100-023-01 CT0254 Homo sapiens cDNA
2078	7192	12436	1.04	4.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
2592	7683	12947	1.2	4.0E-04	Q98815	SWISSPROT	SERICH-2 (SILK GUM PROTEIN 2)
3143	8294	13462	3.12	4.0E-04	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
4300	8422	14584	3.09	4.0E-04	AA576331.1	EST_HUMAN	rh10a10.s1 NCI_CGAP_C01 Homo sapiens cDNA clone IMAGE:951830 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4300	8422	14585	3.09	4.0E-04	AA576331.1	EST_HUMAN	rh10a10.s1 NCI_CGAP_C01 Homo sapiens cDNA clone IMAGE:951830 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4510	9626	14773	2.08	4.0E-04	AA088324.1	EST_HUMAN	zn51 cd8.s1 Stragene muscle 837209 Homo sapiens cDNA clone IMAGE:862670 3'
5072	10173	15308	3.37	4.0E-04	BE660660.1	EST_HUMAN	601345896F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5'
5184	10281	15419	1.76	4.0E-04	Q08848	SWISSPROT	RABPHILIN-3A
161	5348	10480	1.81	3.0E-04	AL119426.1	EST_HUMAN	DKFZ761J221_1 761 (synonym: hary2) Homo sapiens cDNA clone DKFZ761J221 5'
192	5397	10530	1.92	3.0E-04	P49269	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
881	6031	11203	1.8	3.0E-04	U83991.1	NT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1852	6073	12184	1.38	3.0E-04	A1262100.1	EST_HUMAN	qz28d03.y1 NCI CGAP_X1a11 Homo sapiens cDNA clone IMAGE:2028187 5'
1855	6085		2.63	3.0E-04	A1399674.1	EST_HUMAN	h223602.x1 NCI CGAP_F728 Homo sapiens cDNA clone IMAGE:2116082 3'
3280	8438	13538	3.58	3.0E-04	P25147	SWISSPROT	INTERNALIN B PRECURSOR
3938	9072	14228	4.2	3.0E-04	P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4030	9161		1.23	3.0E-04	A1271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
4069	9189		1.08	3.0E-04	BE140808.1	EST_HUMAN	RC0-HT0074-310595-028 HT0014 Homo sapiens cDNA
4785	9888		4.72	3.0E-04	BE153778.1	EST_HUMAN	PM0-HT0388-190200-007-g12 HT0339 Homo sapiens cDNA
171	8366	10507	1.38	2.0E-04	AF217798.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
478	5845	10788	2.85	2.0E-04	AU148707.1	EST_HUMAN	AU148707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
808	6058	11227	8.82	2.0E-04	M86524.1	NT	Human dystrophin gene
808	6058	11228	8.82	2.0E-04	M86524.1	NT	Human dystrophin gene
1181	8318		4.31	2.0E-04	A1266021.1	EST_HUMAN	q188e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
1188	8322		4.78	2.0E-04	AL163203.2	NT	MER3.b2 MER3 repetitive element:
1848	6067		0.99	2.0E-04	AF224288.1	NT	Homo sapiens chromosome 21 segment HS21C003
2106	7279		0.99	2.0E-04	AA478980.1	EST_HUMAN	Mus musculus 5' flanking region of Pib3 gene
							z139b05.s1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains AU repetitive element
2639	7642	12881	2.8	2.0E-04	U68081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV25S1, TCRBV10S1P, TCRBV28S1P, TCRBV18S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRB01, TCRB1S1, TCRB1S2.>
2936	8110	13273	0.83	2.0E-04	A1124529.1	EST_HUMAN	em58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1839780 3'
3318	8463	13828	0.88	2.0E-04	5174796	NT	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3417	8560	13717	2.46	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT0638-070500-194-B07 BT0638 Homo sapiens cDNA
3888	8024	14182	0.87	2.0E-04	AW978441.1	EST_HUMAN	EST390550 IMAGE resequences, MAGP Homo sapiens cDNA
4114	8242		6.91	2.0E-04	U01028.1	NT	Phaeosolus vulgaris nitrate reductase (PVNR2) gene, complete cds
4839	9767	14904	1.35	2.0E-04	H80285.1	EST_HUMAN	y401e11.r1 Soares_pneal_gland_N3HPG Homo sapiens cDNA clone IMAGE:2324550 5'
4638	8757	14905	1.35	2.0E-04	H98295.1	EST_HUMAN	y401e11.r1 Soares_pneal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232558 5'
4784	9877		1.66	2.0E-04	U09226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
5040	10142	16272	1.69	2.0E-04	AB037987.1	NT	Danio rerio hagoromo gene, exons 1 to 6, partial cds
787	5921	11078	1.21	1.0E-04	H99646.1	EST_HUMAN	yc28c09.s1 Soares melanocyte 2Nbl-M Homo sapiens cDNA clone IMAGE:262884 3' similar to contains L1.1 L1 repetitive element:

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1076	6216	11380	2.02	1.0E-04	P11389	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1116	6263	11418	3.41	1.0E-04	AW013947.1	EST_HUMAN	U1H-B10-eab-9-09-Q-JLs1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1115	6253	11417	3.41	1.0E-04	AW013947.1	EST_HUMAN	U1H-B10-eab-9-09-Q-JLs1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708828 3'
1337	8455		3.38	1.0E-04	U62918.1	NT	Arginella arginella dopamine D1A1 receptor (d1A1) gene, complete cds
1638	6767	11860	2.62	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1638	6767	11861	2.62	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1872	6862	12217	1.88	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TC038
3268	8417	13578	0.97	1.0E-04	Q82203	SWISSPROT	SPICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A69)
3717	8555	14009	0.71	1.0E-04	AJ440282.1	EST_HUMAN	U01111.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140289 3' similar to cortactin Ab repetitive element
4034	9165	14307	2.12	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4080	9180	14331	1.38	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLCBB04 3'
5080	10181	16317	1.48	1.0E-04	7682015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5080	10181	16318	1.48	1.0E-04	7682016	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5084	10184	15322	0.92	1.0E-04	AJ357156.1	EST_HUMAN	q62H04.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:2005976 3'
5202	10239	16436	0.97	1.0E-04	AW145147.1	EST_HUMAN	U1H-B13-ell-4-07-Q-JLs1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2798828 3'
696	5853	10998	2.38	9.0E-05	AA718933.1	EST_HUMAN	an45c11.s1 Soares_testes_NHT Homo sapiens cDNA clone 1292488 3'
822	5876	11139	1.19	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
865	6016		7.43	8.0E-05	AJ251646.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
2916	8070		0.77	8.0E-05	M63575.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4480	8578	14716	0.71	8.0E-05	AW044605.1	EST_HUMAN	wy78a04.x1 Soares_NSF_F8_BW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
5201	10288	15435	0.88	8.0E-05	L36918.1	NT	P10 microsatellite DNA (CA repeat)
344	5527	10863	7.12	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220889-011-E04 CT0208 Homo sapiens cDNA
344	5527	10864	7.12	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220889-011-E04 CT0208 Homo sapiens cDNA
506	5731	10859	1.01	7.0E-05	L48075.1	EST_HUMAN	HUM072014F Human fores cDNA Homo sapiens cDNA clone EST HFD072014
506	5731	10860	1.01	7.0E-05	L48075.1	EST_HUMAN	HUM072014F Human fores cDNA Homo sapiens cDNA clone EST HFD072014
1057	6198	11363	1.65	7.0E-05	Q22849	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2680	7177	13027	2.28	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3137	8288	13446	6.92	7.0E-05	AB008080.1	NT	Dictyostelium discoidium gene for TRFA, complete cds
4351	9473	14811	1.84	7.0E-05	AL16201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2020	7137	12376	1.27	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
2020	7137	12377	1.27	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
2550	7683	12903	1.14	6.0E-05	AI855241.1	EST_HUMAN	W554708.x1 NC1_CGAP_G03 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gbJ03286 DNA
2775	6838	10975	2.57	6.0E-05	AF03630.1	NT	TOPOISOMERASE I (HUMAN);
1411	6838	11716	35.84	6.0E-05	AW392088.1	EST_HUMAN	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
1874	6894	14241	1.42	5.0E-05	8923891	NT	QV4-ST0234-241189-040-h11 ST0234 Homo sapiens cDNA
3952	9087	14241	3.47	6.0E-05	AJ251884.1	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55889), mRNA
2768	6419	14717	3.52	4.0E-05	U12821.1	NT	Homo sapiens partial SLC22A3 gene for adrenoreceptor monamine transporter (EMT), exon 1
4461	9580	14718	0.93	4.0E-05	P49183	SWISSPROT	Human nartin (REN) gene, 6' flanking region
4946	9593	14718	0.93	4.0E-05	P49183	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
5004	10108	15238	1.17	4.0E-05	AF164488.1	NT	RETINAL-BINDING PROTEIN (RALBP)
679	6837	10977	0.84	3.0E-05	AJ248081.1	EST_HUMAN	Cryptosporidium parvum isolate Zlatre 15 kDa glycoprotein gp15 gene, partial cds
1060	6201	11365	1.2	3.0E-05	AW273851.1	EST_HUMAN	Drosophila melanogaster senseless protein (sens) gene, complete cds
1132	6269	11431	1.4	3.0E-05	BF037898.1	EST_HUMAN	qf64c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1132	6269	11432	1.4	3.0E-05	BF037898.1	EST_HUMAN	contains Alu repetitive element/contains element KER repetitive element
2882	7779	13029	1.13	3.0E-05	Q82234	SWISSPROT	601461463F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885142 5'
4361	9483	14623	5.96	3.0E-05	BE169211.1	EST_HUMAN	601461463F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885142 5'
4361	9483	14624	5.96	3.0E-05	BE169211.1	EST_HUMAN	SKLEMIN
4446	9694	14705	1.08	3.0E-05	AA36879.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4446	9694	14705	1.08	3.0E-05	AA36879.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4704	9820	14967	1.03	3.0E-05	P97488	SWISSPROT	EST178996 Placenta 1 Homo sapiens cDNA similar to similar to p83-associated protein
4804	5837	10977	0.82	3.0E-05	AJ248081.1	EST_HUMAN	EST178996 Placenta 1 Homo sapiens cDNA similar to similar to p83-associated protein
4811	9823	15064	0.96	3.0E-05	AU125721.1	EST_HUMAN	EST178996 Placenta 1 Homo sapiens cDNA similar to similar to p83-associated protein
2304	7413	12683	1.03	2.0E-05	AJ286021.1	EST_HUMAN	CHEMOKINE RECEPTOR-LIKE 1 (G-PROTEIN COUPLED RECEPTOR DEZ)
2547	7650	12898	1.02	2.0E-05	M13782.1	NT	qf64c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to
2874	7771		3.85	2.0E-05	AA160562.1	EST_HUMAN	contains Alu repetitive element/contains element KER repetitive element
							contains Alu repetitive element/contains element L1 repetitive element

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Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3116	8288	13424	1.28	2.0E-05	BE068038.1	EST_HUMAN	RC3-BT0319-120200-014-008 BT0319 Homo sapiens cDNA
3330	8476	13639	0.68	2.0E-06	AF184914.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3351	8496	13665	0.94	2.0E-05	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
3476	8817		0.82	2.0E-05	X85465.1	NT	S. cerevisiae 12.8 Kbp fragment of fine left arm of chromosome XV
4584	9702	14841	0.63	2.0E-05	AI263349.1	EST_HUMAN	qq13a08.x1 Scores_NH-IMPu_S1 Homo sapiens cDNA clone IMAGE:1832374 3' similar to contains
6010	10113		1.08	2.0E-06	L77688.1	NT	MER18.03 MER18 repetitive element ;
2656	7848	13002	1.15	1.0E-05	AL163282.2	NT	Homo sapiens D1George syndrome critical region, telomeric end
3827	8766	13922	1.84	1.0E-05	AF088273.1	NT	Homo sapiens chromosome 21 segment HS21C082
3790	8927		0.88	1.0E-05	AF223391.1	NT	Drosophila melanogaster strain Lantho 120 Suppressor of Hairless (Su(H)) gene, partial cds
3940	9076	14230	0.21	1.0E-05	P81274	SWISSPROT	Homo sapiens cadherin channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4144	9272	14408	1.2	1.0E-06	AL163203.2	NT	MOSAC PROTEIN LGN
4261	9376	14507	1.84	1.0E-05	AA431118.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
4820	8932	15073	1.81	1.0E-05	AW418134.1	EST_HUMAN	zxc0904.f1 Scores_beds_NHT Homo sapiens cDNA clone IMAGE:781494 5'
4954	10022	16201	0.7	1.0E-06	Z18943.1	NT	xy48g11.x1 NCI_CGAP_Lu04.1 Homo sapiens cDNA clone IMAGE:2856548 3'
2833	7731	12888	2.82	9.0E-06	AI583811.1	EST_HUMAN	H. sapiens repeat region
3089	8222	13373	4.49	9.0E-06	AI216983.1	EST_HUMAN	W73a08.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246388 3'
3594	8733		3.18	9.0E-06	M81755.1	NT	qg11b08.x1 Scores_placenta_8kbwasek_2NbhP8t06W Homo sapiens cDNA clone IMAGE:1759191 3'
2501	7841	12853	3.36	8.0E-06	AW362839.1	EST_HUMAN	Human deoxyglyoxylate aminotransferase (AGXT) gene, exons 1 and 2
680	6126		1.45	7.0E-06	AA689729.1	EST_HUMAN	RC3-CT0269-201189-011-h11 CT0268 Homo sapiens cDNA
1449	6577	11764	3.8	7.0E-06	7682177	NT	ab00710.s1 Strategene lung (8837210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains
2837	7892		6.1	7.0E-06	AI368252.1	EST_HUMAN	MER20.11 MER20 repetitive element ;
3549	8680		1.44	7.0E-06	AA385542.1	EST_HUMAN	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2883	8037	13202	1	6.0E-06	BE069189.1	EST_HUMAN	qv18g09.x1 NCI_CGAP_U03 Homo sapiens cDNA clone IMAGE:1891298 3' similar to contains Alu repetitive element
3689	8808	13955	1.08	6.0E-06	BE069189.1	EST_HUMAN	EST189205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
4718	8081	13232	1.93	6.0E-06	Q01456	SWISSPROT	QV3-BT0378-010300-105-411 BT0378 Homo sapiens cDNA
4726	9839	14983	2.52	6.0E-06	AI040098.1	EST_HUMAN	QV3-BT0379-010300-105-411 BT0378 Homo sapiens cDNA
648	5807	10941	6.07	4.0E-06	R15287.1	EST_HUMAN	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
							cd08e02.x1 Scores_fetal_liver_spleen_INFUS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.12 MER8 repetitive element ;
							yx48c03.f1 Scores infant brain 1N18 Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element ;

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
847	5898	11160	5.54	4.0E-06	AW103354.1	EST_HUMAN	x88g12.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element:
1339	6467	11647	2.81	4.0E-06	AI334628.1	EST_HUMAN	1533609.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1339	6467	11648	2.81	4.0E-06	AI334928.1	EST_HUMAN	1533609.x1 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1485	6812	11799	1.68	4.0E-06	BF355612.1	EST_HUMAN	QV2-NT0046-200900-260-107 NT0046 Homo sapiens cDNA
2245	7356	12873	1.14	4.0E-06	AW016401.1	EST_HUMAN	UHL-BIO-est-4-05-0-UI.1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710426 3'
3036	8190	13346	0.74	4.0E-06	AF188349.1	NT	Gallus gallus Dactyl protein (Dact2) mRNA, complete cds
3871	9007	14163	1.07	4.0E-06	AW848295.1	EST_HUMAN	IL3-CT0214-160200-074-B03 CT0214 Homo sapiens cDNA
4778	8889	15034	2.18	4.0E-06	AI886939.1	EST_HUMAN	w194c10.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element MER22 repetitive element;
2146	7259	12505	0.86	3.0E-06	AA700652.1	EST_HUMAN	2534b08.a1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432683 3' similar to contains L1.11 L1 repetitive element;
2149	7259	12506	0.86	3.0E-06	AA700652.1	EST_HUMAN	2534b08.a1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432683 3' similar to contains L1.11 L1 repetitive element;
2247	7357		1.18	3.0E-06	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
2887	8041	13205	0.94	3.0E-06	AA868218.1	EST_HUMAN	ak48g11.a1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409262 3' similar to contains LTR1.13 LTR1 repetitive element;
3248	8398		2.34	3.0E-06	AI857776.1	EST_HUMAN	w22a05.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2425618 3' similar to TR-O60734 O60734 LINE-1 LIKE PROTEIN; contains L1.12 L1 repetitive element;
3762	8899	14050	1.42	3.0E-06	BE047094.1	EST_HUMAN	hg84d12.x1 NCL_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
3762	8899	14051	1.42	3.0E-06	BE047094.1	EST_HUMAN	hg84d12.x1 NCL_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
4454	9573	14712	0.86	3.0E-06	T50268.1	EST_HUMAN	y078b10.t1 Stratiotes ovary (#637217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
4535	9653	14768	3.81	3.0E-06	X54816.1	NT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus)
189	5394		2.1	2.0E-06	P54369	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID
1582	8711		4.44	2.0E-06	P21414	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
2557	7484	12720	2.79	2.0E-06	AI872138.1	EST_HUMAN	w604603.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297088 3' similar to contains MER30.b1 MER30 repetitive element;
2443	7547	12800	1.72	2.0E-06	P04629	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2834	7637	12865	1.17	2.0E-06	P06719	SWISSPROT	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3504	8845	13811	1.05	2.0E-06	AV657553.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFDB06 3'
3742	8880	14031	1.74	2.0E-06	AA173618.1	EST_HUMAN	z02005.t1 Stratiotes ovarian cancer (#637218) Homo sapiens cDNA clone IMAGE:595232 5'
3753	8890	14041	0.63	2.0E-06	AW450215.1	EST_HUMAN	UI-H-B13-aky-g-05-0-UI.1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736176 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3767	8894	14044	1.44	2.0E-08	AB030898.1	NT	Mus musculus gene for odorant receptor A18, complete cds
32	6243	10389	2.84	1.0E-08	O76082	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
656	6817	10855	1.89	1.0E-06	AF084364.1	NT	Mus musculus DMM5E protein (DMM5e) mRNA, complete cds
1464	6591	11178	1.35	1.0E-08	P09125	SWISSPROT	MEROZOITE SURFACE PROTEIN CMZ-8
1595	6714	11904	1.22	1.0E-08	AA034141.1	EST_HUMAN	208a12.s1 Scarsa_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429882 3' similar to contains Alu repetitive element;
1595	6714	11905	1.22	1.0E-06	AA034141.1	EST_HUMAN	208a12.s1 Scarsa_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429882 3' similar to contains Alu repetitive element;
1697	6728	12346	1.1	1.0E-08	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
1698	7112	12346	3.68	1.0E-08	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
1695	7112	12347	3.68	1.0E-08	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4348	6470	14607	12.92	1.0E-08	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Mol protein (M8604 Mol) gene, complete cds
5098	10168	15327	1.04	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5098	10168	15328	1.04	1.0E-08	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
338	6539	10880	1.19	9.0E-07	AF003528.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
338	6539	10881	1.19	9.0E-07	AF003528.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
4736	8949	14996	4.46	8.0E-07	AI288598.1	EST_HUMAN	q182g07.x1 Scarsa_NHMPV_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
4736	8949	14998	4.46	8.0E-07	AI288598.1	EST_HUMAN	q182g07.x1 Scarsa_NHMPV_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
1915	7034	12254	2.17	6.0E-07	AW855593.1	EST_HUMAN	CM3-CT0277-221089-024-e11 CT0277 Homo sapiens cDNA
2485	7689	12823	2.3	6.0E-07	AF10413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (BF), and complement component C2 (C2) genes>
3945	6061		1.72	6.0E-07	P41479	SWISSPROT	HYPOPHOSPHATASE 1 (HPP1) INTERGENIC REGION
324	6506		1.21	5.0E-07	AB31893.1	EST_HUMAN	Wf64f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
1059	6200		3.61	5.0E-07	A4380630.1	EST_HUMAN	EST636715 Supt cells Homo sapiens cDNA 6' end
3003	6157		0.81	5.0E-07	AB31893.1	EST_HUMAN	Wf64f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
4615	9733	14870	0.98	5.0E-07	AF14974.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
3874	6108	14267	1.94	4.0E-07	AW006602.1	EST_HUMAN	Wf64f10.x1 NCI_CGAP_C33 Homo sapiens cDNA clone IMAGE:2504667 3'
440	5906	10753	3.65	3.0E-07	U19718.1	NT	Human microtubulin-associated glycoprotein (MIFAP2) gene, putative promoter region and alternatively spliced untranslated exons
581	6744	10872	3.16	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1383	6511	11692	1.46	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA

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1637	6768		1.48	3.0E-07	M84857.1	NT	Human IgK subgroup 1 germline gene, exons 1 and 2, V-region 018 allele
2446	7649	12802	19.22	3.0E-07	BE005077.1	EST_HUMAN	MRD-BN0115-020300-001-F11 BN0115 Homo sapiens cDNA
2446	7649	12803	18.22	3.0E-07	BE005077.1	EST_HUMAN	MRD-BN0115-020300-001-F11 BN0115 Homo sapiens cDNA
3008	8160	13317	0.87	3.0E-07	T84704.1	EST_HUMAN	Yd5012.1 Soares fetal liver spleen INFLS Homo sapiens cDNA IMAGE:111695 5'
3138	8289	13446	1.67	3.0E-07	P38739	SWISSPROT	HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4695	9311	14969	7.38	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLC0001 3'
4728	9841	14986	0.72	3.0E-07	AI787238.1	EST_HUMAN	we85b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347867 3'
5046	10148	15277	1.3	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to
6046	10148	15278	1.3	3.0E-07	T57850.1	EST_HUMAN	gb:M62882 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
27	6238	10353	2.63	2.0E-07	AF282888.1	NT	yc14h09.s1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to
149	6346	10483	10.59	2.0E-07	L77689.1	NT	gb:M62882 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
149	6346	10489	10.59	2.0E-07	L77689.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
177	5371	10512	133.71	2.0E-07	U38849.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
747	5603	11057	1.67	2.0E-07	AF003630.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
747	5603	11058	1.67	2.0E-07	AF003630.1	NT	Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds
759	5914		1.10	2.0E-07	P11389	SWISSPROT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
							ENDONUCLEASE]
943	6091	11259	2.03	2.0E-07	AA223260.1	EST_HUMAN	z08607.s1 Stragene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650859 3' similar to gb:U31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element
944	6092	11260	4.36	2.0E-07	T63042.1	EST_HUMAN	yc15g04.s1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:80706 3' similar to contains L1 repetitive element ;
1185	6300	11466	0.92	2.0E-07	Q28768	SWISSPROT	I/6 AUTOANTIGEN
1614	6742	11837	2.37	2.0E-07	Q09701	SWISSPROT	HYPOTHETICAL 72.8 KD PROTEIN C2F7.10 IN CHROMOSOME I
8685	8804	13960	17.85	2.0E-07	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
1103	9241		0.89	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2787	5685	11851	2.67	1.0E-07	P09259	SWISSPROT	GLYCOPROTEIN GPV
3725	6241		0.83	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4269	8393	14531	2.63	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCNF04 6'
4269	8393	14532	2.63	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCNF04 5'
4708	9824		1.46	1.0E-07	O75820	SWISSPROT	ZINC FINGER PROTEIN 189
604	7885		2.32	8.0E-08	AI911362.1	EST_HUMAN	wd16b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1052	6193		0.77	8.0E-08	BE795469.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
3532	6874		1.6	8.0E-08	BE796469.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
77	6288	10428	2.93	7.0E-08	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
1370	6498	11081	30.42	7.0E-08	X04809.1	NT	Rat mRNA for ribosomal protein L31
3563	8704	13884	0.7	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
3563	8704	13886	0.7	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
818	5971	11132	2.76	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
818	5971	11133	2.76	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2343	7450	12705	2.87	6.0E-08	BE144388.1	EST_HUMAN	MRO-HT0168-191169-004-g09 HT0168 Homo sapiens cDNA
3034	8188	13344	0.65	6.0E-08	7682473	NT	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4228	8351	14484	1.03	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
81	5280	10430	2.3	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2217	7329	12582	1.58	6.0E-08	AA493851.1	EST_HUMAN	h03b08.a1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943183 similar to contains Alu repetitive element
1771	6897	12103	1.14	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLID PROTEIN PRECURSOR
1771	6897	12104	1.14	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLID PROTEIN PRECURSOR
2852	8007		1	4.0E-08	AL079591.1	EST_HUMAN	DKFZp434J0426_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434J0426 5'
203	5398		11.08	2.0E-08	AW302988.1	EST_HUMAN	kb8768.x1 NCI_CGAP_Luc28 Homo sapiens cDNA clone IMAGE:2767139 3'
226	5420		6.89	2.0E-08	AA425588.1	EST_HUMAN	2w4807.r1 Scaree_total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element; contains element MER15 repetitive element
499	5953	10789	8.75	2.0E-08	AF198349.1	NT	Gallus gallus Daich2 protein (Daich2), mRNA, complete cds
659	5820	10957	9.78	2.0E-08	AW896438.1	EST_HUMAN	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
659	5820	10958	9.78	2.0E-08	AW896438.1	EST_HUMAN	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
691	6138		32.06	2.0E-08	BE280477.1	EST_HUMAN	601165321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
1348	6477	11657	2.11	2.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
1752	6878		1.38	2.0E-08	BE734871.1	EST_HUMAN	801570483F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3946189 5'
1868	6986		3.08	2.0E-08	AW270271.1	EST_HUMAN	801570483F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3946189 5'
2514	7618		1.57	2.0E-08	K00216.1	NT	Sheep His-rRNA-GUG
3182	8343	13508	5.72	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3182	8343	13507	5.72	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3838	8974		1.56	2.0E-08	AW813620.1	EST_HUMAN	RC3-ST0187-181099-012-503 ST0197 Homo sapiens cDNA
4053	9184	14328	0.65	2.0E-08	U82888.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
4394	9505		2.53	2.0E-08	AA459040.1	EST_HUMAN	aa28607.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.12 L1 repetitive element

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4837	10047		2.73	2.0E-08	AW572881.1	EST_HUMAN	h17h08.x2 NCL CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918327 3' similar to contains Aliu repetitive element
1663	6781	11873	4.03	1.0E-08	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT 1-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1)
1663	6781	11874	4.03	1.0E-08	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT 1-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1)
1785	6911	12116	1.06	1.0E-08	AF126348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
2043	7169		1.82	1.0E-08	BE141968.1	EST_HUMAN	PM2-HT0130-150888-001-112 HT0130 Homo sapiens cDNA
3175	8328	13488	0.95	1.0E-08	BE248844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylar-HGSC project=TCBA Homo sapiens cDNA clone TCBAP6232
3175	8328	13489	0.95	1.0E-08	BE248844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylar-HGSC project=TCBA Homo sapiens cDNA clone TCBAP6232
4221	9346	14478	4.46	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C379
4221	9346	14479	4.46	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C379
3582	8731		1.83	7.0E-09	D86842.1	NT	Homo sapiens DNA for 3-ketoadipyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
3983	9117		0.98	7.0E-09	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
4986	10073	15211	5.03	6.0E-09	BE189421.1	EST_HUMAN	PM1-HT0527-160200-001-105 HT0527 Homo sapiens cDNA
1423	6550	11731	2.7	5.0E-09	BE148284.1	EST_HUMAN	RC2-HT0252-120200-014-110 HT0252 Homo sapiens cDNA
1894	6884	12208	1.01	6.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5183	10261	15399	0.72	5.0E-09	AW605894.1	EST_HUMAN	RC4-HT0251-140100-019-008 HT0251 Homo sapiens cDNA
5183	10261	15400	0.72	5.0E-09	AW605894.1	EST_HUMAN	RC4-HT0251-140100-019-008 HT0251 Homo sapiens cDNA
519	5685		1.52	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
866	9113		2.36	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C085
1481	6608	11794	3	4.0E-09	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
2407	7613	12763	23.69	4.0E-09	AA360878.1	EST_HUMAN	EST58385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 80 kDa
2331	7438	12891	2.77	3.0E-09	BE222239.1	EST_HUMAN	hu08e09.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168120 3' similar to contains MER18.3
3148	8299	13489	3.83	3.0E-09	AW268435.1	EST_HUMAN	MER18 repetitive element
3310	8457	13618	0.94	3.0E-09	BE222239.1	EST_HUMAN	ULH-BW0-4q-q-08-Q.U.11 NCL CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730134 3'
3359	8503		0.61	3.0E-09	AA442272.1	EST_HUMAN	hu08e09.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168120 3' similar to contains MER18.3
4072	9202		0.6	3.0E-09	X16874.1	NT	MER18 repetitive element
4404	8524	14865	3.88	3.0E-09	AF175328.1	NT	244604.11 Soares testis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
							H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
							Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4486	9805	14743	1.47	3.0E-09	Q9Y3R5	SWISSPROT	268.1 KDA PROTEIN C21ORF5 (KIAA0683)
4754	9897	15018	0.98	3.0E-09	AW47832.1	EST_HUMAN	Xy17n02.x1 NCL CGAP_U4 Homo sapiens cDNA clone IMAGE:2863469 3' similar to SW:ELF1_DROME
813	5958		0.64	2.0E-09	X10074.1	NT	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1282	6391	11567	4.89	2.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1871	6800		7.78	2.0E-09	AL118573.1	EST_HUMAN	DKFZp761B1710_f1 761 (synonym: hmy2) Homo sapiens cDNA clone DKFZp761B1710 5'
2307	7416	12668	8.31	2.0E-09	Q9Y3R6	SWISSPROT	268.1 KDA PROTEIN C21ORF5 (KIAA0683)
3910	8048	14205	3.18	2.0E-09	O60241	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
1110	8248	11411	2.27	1.0E-09		NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1110	8248	11412	2.27	1.0E-09	5031824	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1644	6772		0.86	1.0E-09	AJ228041.1	NT	Homo sapiens B59 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2856	8911	13173	1.65	1.0E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p-44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
2891	8948	13209	6.75	1.0E-09	M28659.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
2891	8945	13210	6.75	1.0E-09	M28659.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3010	8164	13321	0.87	1.0E-09	BE535440.1	EST_HUMAN	601058602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3446177 5'
4787	9880		5.33	1.0E-09	AA716297.1	EST_HUMAN	z135b03 at Sources_pined_gland_N31HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
5182	10202	15341	10.98	1.0E-09	T80218.1	EST_HUMAN	ye22c08.r1 Striatogene lung (#637210) Homo sapiens cDNA clone IMAGE:81424 5' similar to contains Alu repetitive element; contains MER28 repetitive element;
1313	6443	11820	1.33	9.0E-10	AW1861740.1	EST_HUMAN	MIR0-SN0040-Q50500-002-c07 SN0040 Homo sapiens cDNA
2786	7952	13118	5.85	9.0E-10	A1870071.1	EST_HUMAN	we78h03.x1 Sources_Dicigratse_cdon_NHCD Homo sapiens cDNA clone IMAGE:2347263 3' similar to SW:RL29_HUMAN_P47914 693 RIBOSOMAL PROTEIN L29; contains element PTR5 repetitive element;
142	5339	10483	8.8	8.0E-10	U63630.2	NT	Homo sapiens MCMA4 (MCMA4) and DNA-PKcs (PRKDC) genes, partial cds
3324	8471	13633	0.93	8.0E-10	BE080748.1	EST_HUMAN	QV1-BT0631-150200-071-01 BT0631 Homo sapiens cDNA
4173	9289	14434	3.5	8.0E-10	A4376832.1	EST_HUMAN	EST88564 Small intestine 1 Homo sapiens cDNA 5' end
699	5858	11003	33.6	7.0E-10	7706226	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
699	5858	11004	33.6	7.0E-10	7706226	NT	Homo sapiens TPA inducible protein (LOC51586), mRNA
1634	6763	11958	1.86	7.0E-10	Q13342	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP-100)
2528	7631		5.19	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3080	8213	13368	2.31	7.0E-10	X00856.1	NT	H. sapiens DHFR gene, exon 3
914	6084	11230	4.11	6.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2639	7737	12990	1.07	6.0E-10	AI424405.1	EST_HUMAN	R02307.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2086021 3'
4707	8823		2.83	6.0E-10	AW853719.1	EST_HUMAN	RC3-CT0254-031089-012-g12 CT0254 Homo sapiens cDNA
760	8916		4.22	6.0E-10	AL046804.1	EST_HUMAN	DKFZp434N219_1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N219 5'
3457	8589	13768	1.18	5.0E-10	Q01033	SWISSPROT	IMPTOTHEICAL GENE 48 PROTEIN
4976	10094	15218	1.16	5.0E-10	AF161897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
107	5311		2.24	4.0E-10	A1221083.1	EST_HUMAN	q02709.x1 Soares_placenta_856wreals_2NbhP889W Homo sapiens cDNA clone IMAGE:176048 3'
579	5742	10870	1.14	4.0E-10	AA616260.1	EST_HUMAN	similar to contains LTR8.b2 LTR8 repetitive element
1897	7114	12349	1.78	4.0E-10	AW584709.1	EST_HUMAN	m04e01.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:924848 3'
2539	7041	12890	2.65	4.0E-10	AL163303.2	NT	hg59g03.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2049844 3' similar to contains Alu repetitive element
916	6095	11232	1.24	3.0E-10	N38113.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
1358	6487		4.89	3.0E-10	AY005160.1	NT	y02708.s1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:272863 3' similar to contains L1.1 L1 repetitive element
34	5245	10381	1.88	2.0E-10	P48988	SWISSPROT	Homo sapiens extracellular glycoprotein lactoferrin precursor, gene, complete cds
34	5245	10382	1.88	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1804	7023		2.47	2.0E-10	U80017.1	NT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
2855	8108		0.93	2.0E-10	BF875047.1	EST_HUMAN	Homo sapiens basilo transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nabp) and survival motor neuron protein (smn) genes, complete cds
1820	6748	11942	2.88	1.0E-10	AV652123.1	EST_HUMAN	602136640F1 NIH_JMGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
2546	7849		2.2	1.0E-10	AW852001.1	EST_HUMAN	QV0-CT0225-181189-058-e08 CT0225 Homo sapiens cDNA
3482	8823	13780	1.85	1.0E-10	AW832912.1	EST_HUMAN	QV2-TT0005-181189-013-g10 TT0003 Homo sapiens cDNA
3527	8639		1.24	1.0E-10	AL041688.1	EST_HUMAN	DKFZp434N1317_1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N1317 5'
3821	8659		1.14	1.0E-10	AL041688.1	EST_HUMAN	DKFZp434N1317_1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N1317 5'
3890	9124		4.88	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4098	8228	14364	6.13	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adenosine diphosphatase protein >
4099	8228	14365	6.13	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTTR), CDM protein (CDM), adenosine diphosphatase protein >
4105	8234	14372	1.92	1.0E-10	AB031069.1	NT	Homo sapiens PCCX1 mRNA for protein containing GXXG domain 1, complete cds
4141	8259		2	1.0E-10	M30629.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
269	5449	10588	0.92	9.0E-11	BE145600.1	EST_HUMAN	IL2-1T0203-281089-018-c08 HT0203 Homo sapiens cDNA
2086	7210	12456	3.33	9.0E-11	AL134393.1	EST_HUMAN	DKFZp547D225.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225.5
2096	7210	12457	3.33	9.0E-11	AL134393.1	EST_HUMAN	DKFZp547D225.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225.5
3384	8509	13877	2.83	9.0E-11	AL134393.1	EST_HUMAN	DKFZp547D225.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225.5
3384	8509	13878	2.83	9.0E-11	AL134393.1	EST_HUMAN	DKFZp547D225.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225.5
4949	10038	15186	1.24	9.0E-11	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3082	8245		7.83	8.0E-11	H19971.1	EST_HUMAN	YNS311.1.1 Soares adult brain N265HB65Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element;
4017	9150	14282	4.86	8.0E-11	N23712.1	EST_HUMAN	YW49608.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:258298 3'
1460	6587	11775	1.38	7.0E-11	AA330642.1	EST_HUMAN	EST84382 Embryo, 6 week 1 Homo sapiens cDNA 5' end
411	5579	10728	5.87	8.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
411	5579	10729	5.87	8.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
11	5222	10334	0.97	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3346	5222	10334	1.38	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4206	9331	14464	1.3	5.0E-11	P48034	SWISSPROT	ALDEHYDE OXIDASE
5189	10286	15422	0.95	5.0E-11	D43770.1	NT	Homo sapiens RNA for differentiation or sex determination
1408	6535		1.16	4.0E-11	AA438042.1	EST_HUMAN	zu01b12.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:730559 5'
2761	7845	13100	4.75	4.0E-11	BE88500.1	EST_HUMAN	601807531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3309285 5'
2839	8083	13260	0.98	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4589	9707	14845	0.88	4.0E-11	D44686.1	EST_HUMAN	HUMSUPY080 Human brain cDNA Homo sapiens cDNA clone 089
1502	6528	11816	9.87	3.0E-11	6878077	NT	Mus musculus expressed in non-malignant cells 2, protein (NM23B) (Nme2), mRNA
4250	9375		1.22	3.0E-11	AA309248.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
981	6109	11278	1.33	2.0E-11	AH50502.1	EST_HUMAN	qt36c04.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1762102 3' similar to contains MER10.15
1187	6321	11490	3.87	2.0E-11	R24807.1	EST_HUMAN	MER10 repetitive element;
1187	6321	11491	3.87	2.0E-11	R24807.1	EST_HUMAN	Y943612.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1628	6754	11947	3.35	2.0E-11	L17492.1	NT	Y943612.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1628	6754	11948	3.35	2.0E-11	L17492.1	NT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and epsilon receptor-like protein
2728	7821	13078	1.04	2.0E-11	AF087613.1	NT	COR3 beta (COR3 beta) genes, complete cds
3179	8330	13494	6.84	2.0E-11	P10263	SWISSPROT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and epsilon receptor-like protein
3307	8454	13816	0.77	2.0E-11	A478617.1	EST_HUMAN	Human endogenous retrovirus HERV-P-T47D
4422	9542		1.16	2.0E-11	BE065637.1	EST_HUMAN	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
							hm54c09.x1 NCL_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2161838 3'
							RC3-BT0318-170200-014-a05 BT0318 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4579	9897		0.85	2.0E-11	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
4912	10022		2.2	2.0E-11	BE082588.1	EST_HUMAN	QV2-B10258-261088-014-01 B10258 Homo sapiens cDNA
4992	10088	16228	0.91	2.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C078
5014	10117	16250	0.62	2.0E-11	AA307331.1	EST_HUMAN	EST1178226 Odon carthagen (HOC) cell line Homo sapiens cDNA 5' end similar to similar to alpha-2-macroglobulin
679	6833	10973	0.63	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
794	6939	11097	1.43	1.0E-11	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1220	6952	11521	2.28	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C078
1513	6940		1.47	1.0E-11	AF119974.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2031	7149	12388	1.31	1.0E-11	P16268	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2118	7233	12478	1.5	1.0E-11	AF00578.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
3480	8021	13786	0.71	1.0E-11	BE004315.1	EST_HUMAN	CMD-BN0105-170300-282-412 BN0105 Homo sapiens cDNA
2918	8072	13242	0.8	9.0E-12	P20742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
4631	9749	14895	1.49	7.0E-12	Q06904	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSMR4)
3534	8978		0.83	6.0E-12	AV730594.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAW06 5'
4325	9447	14980	9.03	6.0E-12	AA732616.1	EST_HUMAN	nz88f11.s1 NCL_CGAP_G081 Homo sapiens cDNA clone IMAGE:1302673 3' similar to cortizone Alu repetitive element
1045	8188	11953	2.75	5.0E-12	T06573.1	EST_HUMAN	EST04482 Fetal brain, Strabagene (cat#338208) Homo sapiens cDNA clone HFB0V33
3371	8516	13883	1.08	6.0E-12	BE047779.1	EST_HUMAN	z62b05.y1 NCL_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2297217 5'
3709	8846	14000	9.31	6.0E-12	AJ271798.1	NT	Homo sapiens Xq pseudocautosomal region; segment 2/2
241	5453	10872	3.41	4.0E-12	AA700326.1	EST_HUMAN	z74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:480878 3'
242	5453	10972	3.98	4.0E-12	AA700326.1	EST_HUMAN	z74g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:480878 3'
4590	9708	14948	0.72	4.0E-12	AI688984.1	EST_HUMAN	z26n05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2220745 3' similar to TR-Q13639 Q13639 MARINER TRANSPOSASE ;
613	5773	10903	3.9	3.0E-12	AW941893.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809377 3' similar to TR-Q14517 Q14517 SMRP ;
613	5773	10904	3.9	3.0E-12	AW941893.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809377 3' similar to TR-Q14517 Q14517 SMRP ;
1666	6784	11989	1.46	2.0E-12	AW802131.1	EST_HUMAN	ILB-UM0071-120400-085-c05 UM0071 Homo sapiens cDNA
3448	8590	13754	0.97	2.0E-12	6784406	NT	h1s musculus keratin-associated protein 6.2 (Krtap6-2), mRNA
4090	9218	14354	2.24	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4090	9218	14355	2.24	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4399	9519		2.08	2.0E-12	BE063509.1	EST_HUMAN	CMD-BT0281-031189-087-003 BT0281 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
118	5310	10462	1.63	1.0E-12	AW627874.1	EST_HUMAN	h90a09.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2870040 3' similar to contains MER18.11 MER18 repetitive element:
1888	7105		1.25	1.0E-12	AB71728.1	EST_HUMAN	hm5107.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2438483 3' similar to contains L1.b3 L1 repetitive element:
3042	8186	13351	0.92	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3042	8188	13352	0.92	1.0E-12	AF000991.1	NT	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3852	8988	14143	27.54	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
3852	8988	14144	27.54	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
3918	9054	14215	0.9	9.0E-13	AB028300.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
716	5872	11019	4.71	8.0E-13	U28185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
715	5872	11020	4.71	8.0E-13	U28185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1851	6972	12163	2.14	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (b2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
2092	7207	12453	0.92	8.0E-13	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
3303	8450		0.61	6.0E-13	R76338.1	EST_HUMAN	y82804.r1 Soares placenta NB2-IP Homo sapiens cDNA clone IMAGE:145759 5'
3378	8523		1.24	6.0E-13	AA435773.1	EST_HUMAN	z77a12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element/contains element MER22 repetitive element:
1878	6988		8.68	4.0E-13	AW378614.1	EST_HUMAN	PM2-HT0224-221099-001-011 HT0224 Homo sapiens cDNA
2437	7641		1.18	4.0E-13	AF003628.1	NT	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions
175	5369		3.66	3.0E-13	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
866	6017		4.09	3.0E-13	AA430310.1	EST_HUMAN	z90508.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:781408 5'
2350	7457	12712	0.98	3.0E-13	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region: segment 2/2
2452	7556		1.57	3.0E-13	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2825	7724	12877	2.84	3.0E-13	BF372882.1	EST_HUMAN	CM3-FT0100-140700-242-H08 FT0100 Homo sapiens cDNA
3169	8320		2.2	3.0E-13	AA745844.1	EST_HUMAN	ob18402.s1 NCL CGAP_K165 Homo sapiens cDNA clone IMAGE:1324035 3'
145	5342	10488	2.57	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT) CDM protein (CDM), adenoleukodystrophy protein >
236	5429	10569	0.95	2.0E-13	U28839.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1274	6403	11577	13.57	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3285	8414	13578	1.13	2.0E-13	BF431899.1	EST_HUMAN	hab7605.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3481	8632	13769	1.19	2.0E-13	AF103607.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4084	9213		1.65	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
289	5477	10616	1.12	1.0E-13	S74128.1	NT	[GIF-1]-fibroblast growth factor 1 [human, kidney, Genomix, 342 nt, segment 2 of 2]
889	6039	11210	3.99	1.0E-13	AJ007873.1	NT	Homo sapiens LGMD2B gene
1341	8489	11660	1.23	1.0E-13	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
2017	7134	12372	8.66	1.0E-13	AA720674.1	EST_HUMAN	nv21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR13 THR repetitive element;
4585	9883	14822	1.57	1.0E-13	BF340987.1	EST_HUMAN	802038009.F1 NCI_CGAP_Bn84 Homo sapiens cDNA clone IMAGE:4165868 5'
331	5514	10651	3.32	9.0E-14	AA781159.1	EST_HUMAN	qj24c01.s1 Scores_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
332	5515	10652	2.87	9.0E-14	AA781159.1	EST_HUMAN	qj24c01.s1 Scores_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
2471	7575		1.95	9.0E-14	AW851577.1	EST_HUMAN	RC4-CT10322-080100-013-409 CT0322 Homo sapiens cDNA
2553	7656	12907	0.89	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2553	7656	12908	0.99	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2717	7812	13067	3.37	9.0E-14	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
3087	8240	13389	4.51	9.0E-14	AW513298.1	EST_HUMAN	xc54h05.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2707833 3'
3223	5514	10651	0.72	9.0E-14	AA781159.1	EST_HUMAN	qj24c01.s1 Scores_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19 repetitive element;
3775	8912	14885	0.58	9.0E-14	D14547.1	NT	Human DNA, SINE repetitive element
4722	8836	14980	1.8	9.0E-14	AJ002153.1	NT	Sagittinus oedipus gene for seminal vesicle secreted protein semenogelin I
3478	8818		1.27	8.0E-14	BE468263.1	EST_HUMAN	hz71c09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
3928	9084		3.4	8.0E-14	R76239.1	EST_HUMAN	MT2c03.r1 Scores_placenta Nb2HP Homo sapiens cDNA clone IMAGE:144798 3'
1639	7922		3.39	7.0E-14	AW151673.1	EST_HUMAN	x87610.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2823148 3' similar to contains MER10.12 MER10 repetitive element;
366	5545	10687	11.15	8.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5 (CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
815	5775	10908	4.88	5.0E-14	Q83120	SWISSPROT	x603605.x1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.12 L1 repetitive element;
5035	10137	15270	1.36	5.0E-14	AW073781.1	EST_HUMAN	
1124	7809		1.65	4.0E-14	P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1898	7008	12228	4.63	4.0E-14	AJ007973.1	NT	Homo sapiens LGM22B gene
3733	8871		0.65	4.0E-14	AA046502.1	EST_HUMAN	2467606.1 Scores_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:487658 5'
4268	9392	14530	0.95	4.0E-14	N46328.1	EST_HUMAN	Y73c12.s1 Scores_multiple_sclerosis_2N4HMSF Homo sapiens cDNA clone IMAGE:279180 3' similar to contains L1.13 L1 repetitive element:
951	6989	11267	1.16	3.0E-14	X95466.1	NT	R_norvegicus mRNA for CPG2 protein
4905	10015	15159	0.65	3.0E-14	AW265354.1	EST_HUMAN	xp45712.x1 NCL_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element:contains element MEF9 repetitive element:
398	5567	10701	2.38	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
398	5567	10702	2.38	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
688	7897	10987	9.97	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2366	7471		1.07	2.0E-14	AW372868.1	EST_HUMAN	RC5-BT0377-091298-031-D12 BT0377 Homo sapiens cDNA
2441	7645		0.98	2.0E-14	7657628	NT	Homo sapiens riboflavin tumor deletion region protein 1 (RTDR1), mRNA
2636	7734		1.07	2.0E-14	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1068	6208	11371	2.48	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
1414	6541	11718	5.76	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1414	6541	11719	5.76	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2002	7119	12355	22.17	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphatase dehydrogenase (G6PD) gene, complete cds
2187	7280	12526	2.46	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2386	7482	12745	23.6	1.0E-14	AF001686.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2910	8064	13236	1.11	1.0E-14	P06227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-II)
3146	8297	13468	5.64	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-409_1 CT0432 Homo sapiens cDNA
3146	8297	13467	5.64	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-409_1 CT0432 Homo sapiens cDNA
3863	8899	14168	1.84	1.0E-14	AA82894.1	EST_HUMAN	aa88c12.s1 Stragena schizo brain S11 Homo sapiens cDNA clone IMAGE:971350 3'
4452	9571	14710	1.81	1.0E-14	AW275952.1	EST_HUMAN	xq39h10.x1 NCL_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2763059 3'
1589	6718	11907	1.49	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2772	5847		1.52	8.0E-15	BE261482.1	EST_HUMAN	601148932F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3184023 5'
695	6141	11310	7.37	6.0E-15	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
409	5577	10725	5.25	5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3450	8592		1.01	5.0E-15	AW268877.1	EST_HUMAN	UHL-BW0-ep-g-10-UJI.s1 NCL_CGAP_Sub Homo sapiens cDNA clone IMAGE:2731219 3'
426	5213	10325	2	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4191	9317		5.22	3.0E-15	N89462.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIODILATIN)

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
247	5438	10578	4.77	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
366	5546	10888	3.58	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
368	5546	10889	3.56	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2352	7459	12714	1.04	2.0E-15	BE350127.1	EST_HUMAN	h08g01.x1 NCI_CGAP_Ku13 Homo sapiens cDNA clone IMAGE:3148258 3' similar to contains MER28.b3 MER29 repetitive element ;
2352	7459	12715	1.04	2.0E-15	BE350127.1	EST_HUMAN	h08g01.x1 NCI_CGAP_Ku13 Homo sapiens cDNA clone IMAGE:3148258 3' similar to contains MER28.b3 MER29 repetitive element ;
3494	8635	13901	0.61	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3494	8635	13902	0.61	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4592	9710		2.53	2.0E-15	AU806335.1	EST_HUMAN	W07708.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q61043 Q61043 NINEIN. ;
2736	7830		2.46	1.0E-15	AJ889884.1	EST_HUMAN	h28h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE. ;
2883	8137	13902	1.71	1.0E-15	BE043584.1	EST_HUMAN	h40e02.y1 NCI_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2899162 5'
3120	8272	13428	1.41	1.0E-15	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4337	9459	14597	0.6	1.0E-15	BE182698.1	EST_HUMAN	RC3-HT0849-100500-022.b05 HT0849 Homo sapiens cDNA
2844	7742	12895	1.04	9.0E-16	Q39610	SWISSPROT	DYNEIN ALPHA CHAIN, FLAGELLAR OUTER ARM
4481	9600	14739	1.04	9.0E-16	4503188	NT	Homo sapiens cut (Drosophila)-like 1 (CCAAT displacement protein) (CUTL1) mRNA
2126	7240		3.12	6.0E-16	AW072611.1	EST_HUMAN	EST384702 IMAGE resequences, MAGL Homo sapiens cDNA
1503	6630	11817	1.38	6.0E-16	AJ251154.1	NT	Mus musculus ciliary receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogenes
2841	7739	12892	1.28	6.0E-16	AA082176.1	EST_HUMAN	o88o04.s1 Soares_tetad_fetus_Nb2Hf8_8w Homo sapiens cDNA clone IMAGE:1623078 3' similar to contains element L1 repetitive element ;
2359	7466	12721	1.04	4.0E-16	AW797168.1	EST_HUMAN	QV1-JM0036-200300-115-g02 UM0036 Homo sapiens cDNA
2359	7466	12722	1.04	4.0E-16	AW797168.1	EST_HUMAN	QV1-JM0036-200300-115-g02 UM0036 Homo sapiens cDNA
3439	8581	13741	3.97	4.0E-16	Q16653	SWISSPROT	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
4113	9241	14377	5.45	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
4113	9241	14378	5.45	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
4928	10036		1.02	4.0E-16	AV730833.1	EST_HUMAN	AV730833 HTF Homo sapiens cDNA clone HTFAXE09 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
128	5326	10472	1.01	3.0E-16	AW022862.1	EST_HUMAN	d145c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2488376 5'
128	5328	10473	1.01	3.0E-16	AW022862.1	EST_HUMAN	d145c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2488376 5'
465	5933		1.3	3.0E-16	AL040445.1	EST_HUMAN	DKFZp434P037.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434P037 5'
475	5842		2.42	3.0E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1465	6592	11780	1.85	3.0E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2846	8099	13263	4.39	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
3906	8042	14202	0.68	3.0E-16	T08169.1	EST_HUMAN	EST00060 Infant Brain, Berto Soares Homo sapiens cDNA clone HIBBA13 5' end
873	8120		1.52	2.0E-16	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
2650	7748		1.74	2.0E-16	J03081.1	NT	Human SSANV-related endogenous retroviral LTR-like element
4149	9276	14412	1.25	2.0E-16	X69211.1	NT	H. sapiens DNA for endogenous retroviral like element
180	5374	10513	2.74	1.0E-16	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
380	5589		21.64	1.0E-16	AA028592.1	EST_HUMAN	af58g11.s1 Soares fetal_Nb2-HF8_5w Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR.12 OFR repetitive element;
1973	7090	12318	2.07	1.0E-16	BF327942.1	EST_HUMAN	QV0-BN0148-070700-283-rt10 BNO148 Homo sapiens cDNA
3720	8868	14011	2.64	9.0E-17	AW800048.1	EST_HUMAN	GM1-NN1003-200300-153-601 NNT003 Homo sapiens cDNA
1019	8180		2.04	8.0E-17	AW880701.1	EST_HUMAN	QV0-O10032-080300-155-d01 OT0032 Homo sapiens cDNA
3859	9005		0.83	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1470	6597		2.64	7.0E-17	6753087	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBec2), mRNA
200	5395	10539	6.46	6.0E-17	AW963880.1	EST_HUMAN	RC1-HN0003-220300-021-504 HN0003 Homo sapiens cDNA
420	5207	10319	2.67	5.0E-17	T64110.1	EST_HUMAN	Y005H08.L1 Stratiogene lung (8937210) Homo sapiens cDNA clone IMAGE:78839 5'
1504	6931		1.25	3.0E-17	D14547.1	NT	Human DNA, SINE repetitive element
2089	7204	12449	1.08	3.0E-17	AW119123.1	EST_HUMAN	cd89cd09.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3'
3177	8328		1.26	3.0E-17	P35410	SWISSPROT	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3620	8769	13915	1.18	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181899 3'
3620	8759	13916	1.18	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181899 3'
350	5533	10672	2.53	2.0E-17	AI270080.1	EST_HUMAN	q163a08.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alb repetitive element;
351	5533	10672	2.82	2.0E-17	AI270080.1	EST_HUMAN	q163a08.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains Alb repetitive element;
889	8136		1.24	2.0E-17	AA72832.1	EST_HUMAN	zg81d04.s1 Soares_fetal_heart_NbHH16W Homo sapiens cDNA clone IMAGE:399751 3'
2424	7529	12781	1.33	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2424	7529	12782	1.33	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2895	8049	13216	6.11	2.0E-17	P12036	SWISSPROT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT
749	5905	11061	2.99	1.0E-17	P08183	SWISSPROT	HEAVY POLYPEPTIDE) (NF-H)
1723	6850		0.98	1.0E-17	AJ271736.1	NT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1778	6904	12112	2.75	1.0E-17	AL163207.2	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2105	7220	12484	1.28	1.0E-17	P02481	SWISSPROT	Homo sapiens chromosome 21 segment HS21C037
2317	7425	12878	1.44	1.0E-17	U76410.1	NT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
3554	8695		0.99	1.0E-17	AF24689.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
4108	8238		7.68	1.0E-17	R09842.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
5185	10282		1.15	1.0E-17	AA28937.1	EST_HUMAN	(UBE2D3) genes, complete cds
3765	8902	14054	1.61	8.0E-18	4758977	NT	Y90407.1 Scores fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:128388 5'
348	5529	10688	40.25	7.0E-18	AW316978.1	EST_HUMAN	EST11498 Uterus Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol
348	5529	10687	40.25	7.0E-18	AW316978.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3277	8426	13587	1.08	6.0E-18	X71791.2	NT	xc10b04.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
4712	9828		3.18	6.0E-18	P62181	SWISSPROT	xc10b04.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
1149	6285	11450	12.11	5.0E-18	AI280214.1	EST_HUMAN	xc10b04.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
120	5320	10463	1.1	4.0E-18	BE044078.1	EST_HUMAN	Rattus norvegicus partial Gdn/Pn-1 gene for gdn-derived nadin/protease nexin 1, enhancer region
120	5320	10464	1.1	4.0E-18	BE044078.1	EST_HUMAN	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSUE TRANSGLUTAMINASE)
1731	6858	12062	30.81	4.0E-18	AA621814.1	EST_HUMAN	(TGase C) (TGC)
850	6001	11173	15.02	3.0E-18	AA814198.1	EST_HUMAN	qm65g11.x1 Scores placenta_8to8weeks_2NBP8b59W Homo sapiens cDNA clone IMAGE:1693668 3'
931	6078	11247	2.16	3.0E-18	BE088834.1	EST_HUMAN	similar to contains Alu repetitive element;
3923	9059	14218	0.68	3.0E-18	AL163247.2	NT	hc36h04.x1 NCI CGAP_UH1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER28 b3
248	5439	10578	3.23	2.0E-18	AW836920.1	EST_HUMAN	MER28 repetitive element;
1154	6280		195.34	2.0E-18	BE250097.1	EST_HUMAN	hc36h04.x1 NCI CGAP_UH1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER28 b3
3100	8253	13403	1	2.0E-18	Q39576	SWISSPROT	hc36h04.x1 NCI CGAP_UH1 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M28328
							keratin, type I cytoskeletal 18 (HUMAN);
							cd23h11.1.1 NCI CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324591 3' similar to SW:RS6_HUMAN
							P46782 40S RIBOSOMAL PROTEIN S5.;
							CMD-BT0690-210300-298-q07 BT0690 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C047
							QV1-L70096-160200-070-e07 LT0096 Homo sapiens cDNA
							60111432F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356044 5'
							DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM

Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4393	8513		0.01	1.0E-18	T85406.1	EST_HUMAN	y643g05.r1 Scores feed liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120538 5' similar to contains L1 repetitive element;
544	5710	10846	4.89	9.0E-19	AA281081.1	EST_HUMAN	z11008.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
545	5710	10846	2.47	9.0E-19	AA281081.1	EST_HUMAN	MER19 repetitive element;
1050	5710	10846	2.47	9.0E-19	AA281081.1	EST_HUMAN	z11008.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
1050	5710	10846	2.47	9.0E-19	AA281081.1	EST_HUMAN	MER19 repetitive element;
2226	7338	12592	2.68	7.0E-19	4758139	NT	EST387007 IMAGE resequences, MAGN Homo sapiens cDNA
3760	8897		1.22	6.0E-19	AW652630.1	EST_HUMAN	Homo sapiens DEADH (Asp-Glu-Ala-AspHis) box polypeptide 6 (RNA helicase, 54KD) (DDX6) mRNA
4442	8561	14703	1.35	6.0E-19	P34986	SWISSPROT	PM0-CT0248-131089-001-g01 CT0248 Homo sapiens cDNA
4442	8561	14704	1.35	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4768	8881		1.48	6.0E-19	AJ271735.1	NT	OLFACTORY RECEPTOR 6 (M50)
5009	10112	15243	1.03	6.0E-19	AL120817.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 1/2
553	6718	10950	0.84	4.0E-19	AB007870.1	EST_HUMAN	DKFZp762F192_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762F192 5'
2843	7741	12984	1.16	4.0E-19	BF697362.1	EST_HUMAN	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
5108	10206		0.88	4.0E-19	AL163208.2	NT	602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5'
3831	8887	14120	1.04	3.0E-19	Q28937	SWISSPROT	Homo sapiens chromosome 21 segment HS21C008
3831	8887	14121	1.04	3.0E-19	Q28937	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4260	8385	14521	0.83	3.0E-19	O43900	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4260	8385	14522	0.83	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4423	8545	14683	1.07	3.0E-19	AV708136.1	EST_HUMAN	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
2529	7632	12880	33.58	2.0E-19	AL163201.2	NT	AV708136 ADC Homo sapiens cDNA clone ADCAMA11 6'
4424	8544		1.43	2.0E-19	AI311783.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001
481	5848		2.72	1.0E-19	BE408611.1	EST_HUMAN	q091e02.x1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q863388 Q863388 POL/ENV GENE;
2146	7260	12507	1.19	1.0E-19	H30795.1	EST_HUMAN	601304126F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
2678	7776		1.37	1.0E-19	D38044.1	NT	y678g07.r1 Scores adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains
2810	7968		5.49	1.0E-19	4758977	NT	MER10 repetitive element;
3382	8526	13688	1.25	1.0E-19	AA834887.1	EST_HUMAN	Human gene for Ahr-receptor, exon 7-9
3268	8408	13571	0.89	7.0E-20	BF328455.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3542	8883	13846	3.35	6.0E-20	P33188	SWISSPROT	q461x12 s1 Scores testis_NHT Homo sapiens cDNA clone IMAGE:1383631 3' similar to contains MER37.12
							MER37 repetitive element;
							PM4-AN0096-050900-003-a04 AN0096 Homo sapiens cDNA
							ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY

Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4246	8371	14504	2.93	8.0E-20	BE02494.1	EST_HUMAN	601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
4568	8888		1.46	5.0E-20	AV725123.1	EST_HUMAN	AV725123 HTC Homo sapiens cDNA clone HTC81A01 5'
1832	6761	11967	1.38	4.0E-20	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4182	8308	14445	1.38	3.0E-20	P23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 114
4594	9712	14849	0.93	3.0E-20	AA037816.1	EST_HUMAN	ZK6612.81 Soares_pregnant_uterus_NHHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.13 L1 repetitive element;
831	5883		20.38	2.0E-20	AW303868.1	EST_HUMAN	X724910.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2781088 3' similar to SW_RS5_MOUSE
1112	8250	11413	2.88	2.0E-20	AA516335.1	EST_HUMAN	ng93109.s1 NCI_CGAP_Lp2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224088
1112	8250	11414	2.96	2.0E-20	AA516335.1	EST_HUMAN	ng93109.s1 NCI_CGAP_Lp2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224088
2778	5883		12.94	2.0E-20	AW303868.1	EST_HUMAN	G1224088 ORF2: FUNCTION UNKNOWN. ;
4923	10033	15174	3.78	2.0E-20	Q26983	SWISSPROT	ng93109.s1 NCI_CGAP_Lp2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224088
4923	10033	15176	3.78	2.0E-20	Q26983	SWISSPROT	G1224088 ORF2: FUNCTION UNKNOWN. ;
6124	10226		1.16	2.0E-20	6174638	NT	X724910.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2781088 3' similar to SW_RS5_MOUSE
2010	7874	12384	1.86	1.0E-20	AA281981.1	EST_HUMAN	P97461.40S RIBOSOMAL PROTEIN S6. ;
4416	8538	14976	0.94	1.0E-20	BF115158.1	EST_HUMAN	ZONADHESIN PRECURSOR
2878	8632		0.97	9.0E-21	AJ003514.1	EST_HUMAN	ZONADHESIN PRECURSOR
2081	7177	12415	2.98	7.0E-21	P15800	SWISSPROT	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
2081	7177	12416	2.98	7.0E-21	P15800	SWISSPROT	211408.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
3679	8818	13976	0.6	7.0E-21	AL183300.2	NT	repetitive element;
4231	8358		6.25	7.0E-21	AA046502.1	EST_HUMAN	repetitive element;
4078	8208	14346	0.6	6.0E-21	BE408611.1	EST_HUMAN	h84608.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1
829	6073	11241	0.69	6.0E-21	5802031	NT	AJ003514 Selected chromosome 21 cDNA library Hairo sapiens cDNA clone M7P12-8J21
4341	9483	14800	2.97	5.0E-21	BE568839.1	EST_HUMAN	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
4770	9883	15030	7.42	5.0E-21	4885474	NT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
1747	6873	12078	1.2	4.0E-21	AA970713.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
2253	7363	12619	1.05	3.0E-21	AL163201.2	NT	2467a08.r1 Soares_pregnant_uterus_NHHPU Homo sapiens cDNA clone IMAGE:487858 5'
3052	8206	13360	3.39	3.0E-21	AJ007873.1	NT	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:369310 5'
							Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
							601649871F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3633680 5'
							Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
							cd66e08.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16530 Q16530
							PM55 MRNA ; contains ORF.11 ORF repetitive element;
							Homo sapiens chromosome 21 segment HS21C001
							Homo sapiens LGMD2B gene

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Table 4

Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
141	6338		19.37	2.0E-21	BE163247.1	EST_HUMAN	QV3-HT0468-17020-090-g12 HT0468 Homo sapiens cDNA
936	6094	11249	0.95	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
936	6094	11250	0.95	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1217	6348		2.95	2.0E-21	BE064410.1	EST_HUMAN	RC4-BT0311-141189-011-H08 BT0311 Homo sapiens cDNA
2601	7701	12846	1.72	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2601	7701	12857	1.72	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
1259	6358	11565	1.63	1.0E-21	AA557657.1	EST_HUMAN	n46-c04.a1 NCL_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER28.b2
1410	6637		2.71	1.0E-21	AB001284.1	EST_HUMAN	MER29 repetitive element;
4388	9508	14650	2.25	9.0E-22	AI702438.1	EST_HUMAN	air68d12.x1 Barleed codon HPLRBT Homo sapiens cDNA clone IMAGE:2162343 3'
950	6098		5.92	8.0E-22	BE144748.1	EST_HUMAN	ts24a03.x1 NCL_CGAP_K111 Homo sapiens cDNA clone IMAGE:2286204 3' similar to TR:Q15408 Q15408
694	5824	10982	4.97	7.0E-22	AL163248.2	NT	NEUTRAL PROTEASE LARGE SUBUNIT;
4267	9382	14515	1.84	7.0E-22	Q61838	SWISSPROT	Homo sapiens chromosome 21 segment HS21CQ48
5020	10122	15254	1.06	7.0E-22	AB008691.1	NT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
4035	9168	14308	1.01	8.0E-22	AA405040.1	EST_HUMAN	Homo sapiens gene for actinin receptor type IIB, complete cds
3614	8753		1.26	4.0E-22	AJ271736.1	NT	z165d10.1 Scores_basla_NHT Homo sapiens cDNA clone IMAGE:742867 5'
960	6108		0.93	3.0E-22	AI468878.1	EST_HUMAN	(Homo sapiens Xq pseudautosomal region; segment 1/2
2535	7698	12866	2.31	3.0E-22	AB59038.1	EST_HUMAN	tm14h10.x1 NCL_CGAP_Cot14 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gbl:19593 HIGH
3650	8789		1.46	3.0E-22	D14718.1	NT	AFFINITY INTERLEUKIN-3 RECEPTOR B (HUMAN) contains L1.11 L1 repetitive element;
4769	9882	15028	2.88	3.0E-22	AI090125.1	EST_HUMAN	wf6504.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428639 3' similar to SW:RL21_HUMAN
1857	7074		1.38	2.0E-22	N24942.1	EST_HUMAN	P46778 60S RIBOSOMAL PROTEIN L21.;
2495	7589	12847	1.32	2.0E-22	P24916	SWISSPROT	Human chromosomal protein HM01 related gene
3401	8545	13704	3.71	2.0E-22	8394043	NT	qb28c07.x1 Scores_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697680 3' similar to
4203	9328	14460	1.73	2.0E-22	AW61784.1	EST_HUMAN	contains MER1212 MER12 repetitive element;
1889	7009	12228	1.11	1.0E-22	AW865517.1	EST_HUMAN	yx73d05.a1 Scores melanocyte 2X1b-IM Homo sapiens cDNA clone IMAGE:267359 3'
3392	8536	13697	1.42	1.0E-22	D14547.1	NT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
3567	8638	13658	0.6	8.0E-23	AF168349.1	NT	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
3292	9439		2.2	7.0E-23	AV847249.1	EST_HUMAN	Human DNA, SINE repetitive element
3415	8558		1.77	8.0E-23	AF168333.1	NT	Gallus gallus Dact12 protein (Dact12) mRNA, complete cds
4242	9357	14500	1.08	8.0E-23	AL163249.2	NT	AV647246 GLC Homo sapiens cDNA clone GLCAW C07 3'
							Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
							Homo sapiens chromosome 21 segment HS21CQ48

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Table 4
Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
665	5826	10963	3.85	2.0E-23	AJ289880.1	NT	Homo sapiens KIAA0861 gene (partial), X13 gene and LZTFL1 gene
1144	7888		3.08	2.0E-23	M55270.1	NT	Human matrix Gla protein (MGp) gene, complete cds
2759	7850	13105	1.39	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2759	7850	13108	1.39	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
3353	8498		0.87	2.0E-23	AI201488.1	EST_HUMAN	q73f11.1 NCJ CGAP_P28 Homo sapiens cDNA clone IMAGE:1843767 3' similar to TR:Q13537 Q13537
3353	8498		0.87	2.0E-23	AI201488.1	EST_HUMAN	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE ;
3353	8498		0.87	2.0E-23	AI201488.1	EST_HUMAN	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE ;
3949	9084	14237	2.51	2.0E-23	H59931.1	EST_HUMAN	Y16a02.1 Sources fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
3949	9084	14238	2.51	2.0E-23	H59931.1	EST_HUMAN	Y16a02.1 Sources fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
4003	9822	14764	1.68	1.0E-23	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
4731	9844		6.27	1.0E-23	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
551	5716		3.88	9.0E-24	AA683213.1	EST_HUMAN	ab75a06.s1 Strabagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:862768 3' similar to
4817	9735	14872	1.03	8.0E-24	P23269	SWISSPROT	TRE18922 E18922 CA PROTEIN ;
4817	9735	14873	1.03	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 13
3850	8986		1.12	7.0E-24	AW537864.1	EST_HUMAN	OLFACTORY RECEPTOR-LIKE PROTEIN 13
704	8991		2.18	6.0E-24	AB001421.1	NT	QV0-DT0047-170200-122-a08 D10047 Homo sapiens cDNA
839	8991	11169	14.22	6.0E-24	AL163249.2	NT	Macaca fascicularis mRNA for Testis-Specific Protein Y (TSPY), complete cds
3943	8079	14232	7.47	5.0E-24	AJ229043.1	NT	Homo sapiens chromosome 21 segment HS21C049
6076	10176	16310	1.58	3.0E-24	F08337.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C049
2326	7434	12687	1.07	2.0E-24	AA197839.1	EST_HUMAN	HSCZRC061 normalized infant brain cDNA Homo sapiens cDNA clone IMAGE:21q22, segment 3/3
3778	8913		0.88	2.0E-24	AW598189.1	EST_HUMAN	zpl110a.1 Strabagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:209161 5'
1709	8837	12038	3.43	1.0E-24	7708340	NT	RC3-NN0088-090500-021-503 NN0088 Homo sapiens cDNA
2634	7732		1	1.0E-24	AW820194.1	EST_HUMAN	Homo sapiens CG1-127 protein (LOC61849), mRNA
2902	8147	13307	0.65	1.0E-24	D88423.1	NT	QV0-ST0294-100400-185-c10 ST0294 Homo sapiens cDNA
4244	9369		1.97	1.0E-24	AF143313.1	NT	Mus musculus mRNA for HGT keratin, partial cds
5182	10279	15417	1.03	9.0E-25	AW857138.1	EST_HUMAN	Homo sapiens PTEN (PTEN) gene, exon 2
4982	10090	15223	3.25	7.0E-25	AA148394.1	EST_HUMAN	RC1-C10302-040400-017-c02 C10302 Homo sapiens cDNA
1694	6792	11988	1.32	5.0E-25	AW850271.1	EST_HUMAN	ne92a10.s1 NCJ CGAP_Klot Homo sapiens cDNA clone IMAGE:911764 similar to contains MER1.52
1459	6568	11774	1.45	4.0E-25	T88107.1	EST_HUMAN	MER1 repetitive element ;
3383	8527		3.48	4.0E-25	AW887871.1	EST_HUMAN	IL3-CT0219-161189-031-D04 CT0219 Homo sapiens cDNA
4294	9418		3.86	4.0E-25	BE170957.1	EST_HUMAN	y65f04.1 Sources fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121783 5'
3301	8448	13610	2.96	3.0E-25	8923321	NT	PLV3-OT0093-280200-001-g07 OT0093 Homo sapiens cDNA
							QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA
							Homo sapiens hypothetical protein FLJ20344 (FLJ20844), mRNA

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3301	8448	13811	2.08	3.0E-26	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
1354	6483	11603	3.09	2.0E-26	6032168	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2286	7384	12845	4.17	2.0E-26	BE88018.1	EST_HUMAN	601811330F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
2782	7617	12858	8.6	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4191	9287	14423	1.6	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4181	9287	14423	1.6	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
362	5542	10684	0.96	1.0E-26	AL040229.1	EST_HUMAN	DKFZp434f0313 J1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434f0313 5'
1262	6382	12768	1.96	1.0E-25	8836487	NT	Human endogenous retrovirus, complete genome
2412	7518	12768	2.79	1.0E-26	Q06056	SWISSPROT	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C)
4828	9940	16082	2.68	1.0E-26	BE162737.1	EST_HUMAN	PM1-HT0464-080100-002409 HT0464 Homo sapiens cDNA
2458	7500	12612	1.08	9.0E-26	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C016
1690	6719	11608	1.3	7.0E-26	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 end flanking repeat regions
3953	6088	14242	1.18	7.0E-26	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
4131	6269	14396	1.87	7.0E-26	AW340153.1	EST_HUMAN	h02012.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2808368 3'
2207	7319	12670	2.86	8.0E-26	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
3328	8474	13637	1	6.0E-26	AA208131.1	EST_HUMAN	z352h04.r1 Strategene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:845271 5'
1179	6314	11482	1.72	5.0E-26	AI708235.1	EST_HUMAN	es38h08.x1 Barslead acra HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP-F49C12.11 CE03371 ;
1179	6314	11483	1.72	6.0E-26	AI708235.1	EST_HUMAN	es38h08.x1 Barslead acra HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP-F49C12.11 CE03371 ;
1668	6887		1.21	4.0E-26	AA329548.1	EST_HUMAN	EST33448 Embryo, 12 week II Homo sapiens cDNA 5' end
1770	6898	12102	0.96	3.0E-26	D14647.1	NT	Human DNA, SINE repetitive element
2004	7121	12357	1.15	3.0E-26	AL045855.2	EST_HUMAN	DKFZp434f068 J1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434f068 5'
2026	7143		2.18	3.0E-26	AA119895.1	EST_HUMAN	z330d08.r1 Strategene neuroepithelium NT2RAM1 837234 Homo sapiens cDNA clone IMAGE:848943 5' similar to gb:MH4338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3759	8398	14040	1.26	3.0E-26	AA152464.1	EST_HUMAN	z330f10.r1 Strategene colon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR-G698374
3759	8398	14047	1.25	3.0E-26	AA152464.1	EST_HUMAN	G698374 THYROID RECEPTOR INTERACTOR ;
680	5938	10978	5.51	2.0E-26	AL163282.2	NT	G698374 THYROID RECEPTOR INTERACTOR ;
1879	6869		1.73	2.0E-26	AL030099.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
3216	6367	13631	6.31	2.0E-26	X86894.1	NT	DKFZp568l171.s1 568 (synonym: htkd2) Homo sapiens cDNA clone DKFZp568l171 3'
							M.musculus mRNA for astrocytic phosphoprotein, PEAA-15

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
132	6330	10476	40.20	1.0E-26	BE170371.1	EST_HUMAN	QV4HT0538-020300-123-a02 HT0538 Homo sapiens cDNA
2532	7635	12883	0.95	1.0E-26	BE814995.1	EST_HUMAN	MIR2-BN0114-240500-030-g07 BN0114 Homo sapiens cDNA
2648	7748		25.15	1.0E-28	AF281085.1	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds
10	5221	10333	3.06	8.0E-27	AI831482.1	EST_HUMAN	wf4bc04.x1 NCI_CGAP_Lu18 Homo sapiens cDNA clone IMAGE:2408160 3' similar to contains THR.b2 THR repetitive element:
558	5721		4.14	8.0E-27	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1424	6551	11732	72.92	8.0E-27	AW162737.1	EST_HUMAN	eu87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783285 3' similar to gb:K00659 TUBULIN ALPHA-1 CHAIN (HUMAN);
1424	6551	11733	72.92	8.0E-27	AW162737.1	EST_HUMAN	eu87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783285 3' similar to gb:K00659 TUBULIN ALPHA-1 CHAIN (HUMAN);
2149	7232	12510	1.86	8.0E-27	AW864776.1	EST_HUMAN	PM2-SN0018-220300-002-a07 SN0018 Homo sapiens cDNA ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3168	8317	13479	2.34	8.0E-27	P12236	SWISSPROT	Human endogenous retroviral element HC2
682	6940		2.02	7.0E-27	Z70684.1	NT	Human endogenous retroviral element HC2
6074	10175		2.28	7.0E-27	AW628172.1	EST_HUMAN	h151h12.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2875879 3' similar to TR:O76040 O76040 ORF2: FUNCTION UNKNOWN.;
2362	7469	12724	2.17	4.0E-27	D25303.1	NT	Human mRNA for Integrin alpha subunit, complete cds
2033	7153	12983	2.58	3.0E-27	X60658.1	NT	Rattus RYAS mRNA for a potential ligand-binding protein
4245	6370	14503	1.31	3.0E-27	BE071924.1	EST_HUMAN	PM0-BT0527-090100-001-d11 BT0527 Homo sapiens cDNA
40	5251	10369	28.98	2.0E-27	AF054197.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1902	7021		45.43	2.0E-27	AA565345.1	EST_HUMAN	h1401b10.s1 NCI_CGAP_Prl1 Homo sapiens cDNA clone IMAGE:1000609 similar to gb:M17889 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
3085	8238		10.92	2.0E-27	AW628172.1	EST_HUMAN	h151h12.x1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2875879 3' similar to TR:O76040 O76040 ORF2: FUNCTION UNKNOWN.;
3209	8960	13521	2.17	2.0E-27	AF111187.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3209	8960	13522	2.17	2.0E-27	AF111187.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
435	5504		1.48	1.0E-27	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046 Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
997	6143	11311	1.58	1.0E-27	AB028899.1	NT	Homo sapiens xylidkinase (H. Influenzae) homolog (XYLB) mRNA
1711	6839	12040	0.87	1.0E-27	4827059	NT	h108g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b2 MER29 repetitive element:
4058	9189		0.93	1.0E-27	BE350127.1	EST_HUMAN	

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
137	5333		1.88	9.0E-28	BE348398.1	EST_HUMAN	hw17c11.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314 SECRETED NEUREXIN III-ALPHA-C PRECURSOR [3] TR:Q07280 TR:Q07313;
309	5495	10635	2.48	9.0E-28	AU128280.1	EST_HUMAN	AU128280 NT2RP1 Homo sapiens cDNA clone NT2RP1000443 5'
5144	10244	15381	1.58	9.0E-28	AI590115.1	EST_HUMAN	bt12b09.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.L1 OFF repetitive element;
5144	10244	15382	1.58	9.0E-28	AI590115.1	EST_HUMAN	bt12b09.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.L1 OFF repetitive element;
1183	6318	11488	12.92	7.0E-28	AU142750.1	EST_HUMAN	AU142750 Y78A41 Homo sapiens cDNA clone Y78A41000824 5'
316	5502		2.47	5.0E-28	AI921003.1	EST_HUMAN	wt18c07.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2465692 3' similar to contains THR.b1 THR repetitive element;
3984	9118	14265	1.27	5.0E-28	R78782.1	EST_HUMAN	y88f10.J1 Scores placenta NB2-IP Homo sapiens cDNA clone IMAGE:148443 5'
2590	7691	12946	1.78	4.0E-28	AW195086.1	EST_HUMAN	xt33c08.x1 NCL_CGAP_KM11 Homo sapiens cDNA clone IMAGE:2695504 3' similar to SW:GG85_HUMAN Q08378 GOLGIN-95;
2946	8100	13284	1.43	4.0E-28	4505316	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
3084	8237	13387	2.63	4.0E-28	BE409100.1	EST_HUMAN	601300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635305 5'
1287	6416		1.61	3.0E-28	AF153382.1	NT	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
6100	10200		0.92	3.0E-28	AF008680.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S8A2 to TCRBV12S2 region
84	5293	10433	9.51	2.0E-28	BE082107.1	EST_HUMAN	RC1-BT0254-220300-019-005 BT0254 Homo sapiens cDNA
1167	6302	11488	7.61	2.0E-28	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
2450	7554	12808	2.09	2.0E-28	AI348834.1	EST_HUMAN	qc35b06.x1 NCL_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1 repetitive element;
3343	8489	13655	0.62	2.0E-28	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C003
1488	6615	11803	2.07	1.0E-28	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2202	7314	12568	1.03	1.0E-28	BF333236.1	EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
4541	9689		0.88	1.0E-28	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
1616	6744	11939	1.25	7.0E-28	AW96447.1	EST_HUMAN	EST1378521 IMAGE resequences, MAGI Homo sapiens cDNA
693	5755	10893	8.3	6.0E-28	AI936748.1	EST_HUMAN	wp88b01.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2468985 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN, contains LTR7.b1 LTR7 repetitive element;
4984	10092		1.32	5.0E-28	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
3217	8388		2.16	4.0E-28	AI762387.1	EST_HUMAN	ont15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_ont15c02 random
4392	9512	14654	1.32	3.0E-28	AB042287.1	NT	Homo sapiens PTPS gene for 6-pyruvoyltransferin synthase, complete cds
4701	9817	14965	1.08	3.0E-28	BF333236.1	EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
492	5659	10794	2.02	2.0E-29	AF084869.1	NT	Homo sapiens envelope protein RIC-8 (env) gene, complete cds
492	5659	10795	2.02	2.0E-29	AF084869.1	NT	Homo sapiens envelope protein RIC-8 (env) gene, complete cds
1547	6876	11860	6.63	2.0E-29	AI983604.1	EST_HUMAN	wf65d10.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15548 O15548 HERV-E ENVELOPE GLYCOPROTEIN;
1547	6875	11861	5.63	2.0E-29	AI983604.1	EST_HUMAN	wf65d10.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15548 O15548 HERV-E ENVELOPE GLYCOPROTEIN;
4253	9378	14509	2.04	2.0E-29	AL183298.2	NT	Homo sapiens chromosome 21 segment HS21C088
1530	6657	12117	2.08	7.0E-30	BE091133.1	EST_HUMAN	PM4-B10724-150400-004-d11 BT0724 Homo sapiens cDNA
1783	6809	12117	1.11	8.0E-30	D29303.1	NT	Human mRNA for Integrin alpha subunit, complete cds
3173	8324	13485	3.1	8.0E-30	BE008028.1	EST_HUMAN	QV0-BN0147-290400-214-F12 BN0147 Homo sapiens cDNA
4724	8324	13485	0.94	8.0E-30	BE008028.1	EST_HUMAN	QV0-BN0147-290400-214-F12 BN0147 Homo sapiens cDNA
3988	9122	14269	30.82	5.0E-30	AI386992.1	EST_HUMAN	ig82g03.x1 NCI_CGAP_CL1.1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Abu repetitive element;
2128	7242	12484	1.89	4.0E-30	AW637471.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
2128	7242	12485	1.89	4.0E-30	AW637471.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
1153	6289		2.88	3.0E-30	AI386551.1	EST_HUMAN	qq83c05.x1 Scarses_fetal_fetus_Nb2HFB_gw Homo sapiens cDNA clone IMAGE:1838920 3' similar to contains MER29.k2 MER29 repetitive element;
3738	8876	14027	0.93	3.0E-30	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exon 1-9
674	5932	10972	1.27	2.0E-30	AW857315.1	EST_HUMAN	GMD-CT0307-310100-159-H03 CT0307 Homo sapiens cDNA
1085	6224		1.82	2.0E-30	F08888.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
1469	6616	11804	3.7	2.0E-30	BE176977.1	EST_HUMAN	RC6-HT0682-110400-013-H08 HT0682 Homo sapiens cDNA
2876	7773	13024	4.7	2.0E-30	BE176977.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
2885	8039	13204	7	2.0E-30	AF114156.1	NT	Homo sapiens Y-linked zinc finger protein (ZFP) gene, complete cds
3768	8905	14088	2.23	2.0E-30	AW206581.1	EST_HUMAN	UH-B11-460-c-12-QJL.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4745	8858	15008	3.09	2.0E-30	BE288945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
4745	8858	15007	3.09	2.0E-30	BE288945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029438 5'
284	6473	10815	14.45	1.0E-30	C18839.1	EST_HUMAN	G18938 Human placenta cDNA (TF11/jwara) Homo sapiens cDNA clone GEN-570C01 5'
536	5702	10835	7.24	1.0E-30	AW489897.1	EST_HUMAN	hd30b04.x1 Scarses_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1.13 MER1 repetitive element;
714	6871	11018	3.43	1.0E-30	AL183293.2	NT	Homo sapiens chromosome 21 segment HS21C003
2184	7305	12566	2.77	1.0E-30	AA664377.1	EST_HUMAN	ac77608.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:988569 3'
2438	7542	12785	1.44	1.0E-30	BF947728.1	EST_HUMAN	60202260F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4167891 5'
2874	8128	13291	1.24	1.0E-30	5803081	NT	Homo sapiens methionine aminopeptidase 1F-2-associated p67 (MINPEP), mRNA
3029	8180	13336	0.87	1.0E-30	AA316045.1	EST_HUMAN	EST188868 HCC cell line (metastasis to liver in mouse) Homo sapiens cDNA 5' end

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3746	8884	14034	0.8	9.0E-31	T73025.1	EST_HUMAN	yc65608.t1 Stratagene liver (#637224) Homo sapiens cDNA clone IMAGE:85570 5'
3746	8884	14035	0.6	9.0E-31	T73025.1	EST_HUMAN	yc65608.t1 Stratagene liver (#637224) Homo sapiens cDNA clone IMAGE:85570 5'
1078	6218	11383	6.59	8.0E-31	8923389	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
2380	7488		8.16	8.0E-31	AL103208.2	NT	Homo sapiens chromosome 21 segment HS21C008
4895	10006	15150	0.98	8.0E-31	P23275	SWISSPROT	OLFACTORY RECEPTOR 15 (OR3)
4895	10006	15151	0.88	8.0E-31	P23275	SWISSPROT	OLFACTORY RECEPTOR 15 (OR3)
709	5868		1.37	7.0E-31	AA372637.1	EST_HUMAN	ESTB4555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
2628	7727	12882	2.1	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCL CGAP Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2628	7727	12883	2.1	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCL CGAP Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
3659	8795		2.31	6.0E-31	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
189	5384	10628	2.84	5.0E-31	M60894.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
189	5384	10627	2.84	5.0E-31	M60894.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
594	5766		3.28	4.0E-31	AJ271755.1	NT	Homo sapiens Xa pseudoscutellon region, segment 1/2
1824	8752	11945	1.08	4.0E-31	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
1828	8952		1.27	4.0E-31	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2750	7844		1.87	4.0E-31	5730038	NT	Homo sapiens SET domain and matrin transposase fusion gene (SETMAR) mRNA
2558	7680	12813	2.37	3.0E-31	6006871	NT	Homo sapiens SEC23, endoplasmic reticulum transmembrane component (S. cerevisiae) like (SEC23L), mRNA
1920	7039	12280	1.98	2.0E-31	AW838171.1	EST_HUMAN	QV2-LT0051-260300-111-103 LT0051 Homo sapiens cDNA
2188	7308	12558	1.54	2.0E-31	A1893388.1	EST_HUMAN	g44905.x1 Scarsa_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111672 3'
2321	7428	12682	0.98	2.0E-31	AL119248.1	EST_HUMAN	DKFZp781G1613.t1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781G1613 5'
2418	7523	12776	3.48	2.0E-31	AA488824.1	EST_HUMAN	aa88f11.a1 Stratagene fetal retina 887202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR12 THR repetitive element;
15	5226	10339	5.7	1.0E-31	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
1676	6805	12000	7.87	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1676	6805	12001	7.87	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1676	6805	12002	7.87	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
4605	9723	14857	1.1	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235.t1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547B235 5'
4605	9723	14858	1.1	1.0E-31	AL134376.1	EST_HUMAN	DKFZp547B235.t1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547B235 5'
2828	7893		1.08	9.0E-32	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2089	7185	12426	6.64	8.0E-32	AI056770.1	EST_HUMAN	oz15a09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675384 3'
4828	8941	15083	0.94	7.0E-32	P62691	SWISSPROT	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P146)
1036	8177	11342	48.23	5.0E-32	AF110027.1	NT	Homo sapiens PRO1181 mRNA, complete cds
932	5080		1.85	4.0E-32	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
465	5623	10768	3.08	3.0E-32	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1467	6594	11763	16.88	3.0E-32	AV731500.1	EST_HUMAN	AV731500 HTF Homo sapiens cDNA clone HTFAK007 5'
2873	8027	13194	0.64	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q23) (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2873	8027	13185	0.64	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q23) (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
2838	7738		1.98	1.0E-32	DB4430.1	NT	Homo sapiens mRNA for phenylalanine RNA synthetase, complete cds
3087	8220		1.47	1.0E-32	BE743298.1	EST_HUMAN	601573207F1 NIH MGC 9 Homo sapiens cDNA clone IMAGE:3834433 5'
3482	8604		5.35	9.0E-33	BE327112.1	EST_HUMAN	hw07a05.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:O88539 O88539 WW DOMAIN BINDING PROTEIN 11.;
60	5271	10403	5.57	7.0E-33	5031738	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
60	5271	10404	5.57	7.0E-33	5031738	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2143	7257	12503	1.13	7.0E-33	AI590115.1	EST_HUMAN	bt12608.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.H OFF repetitive element;
2810	7709		5.84	7.0E-33	AV730058.1	EST_HUMAN	AV730058 HTF Homo sapiens cDNA clone HTFAVE08 5'
3226	8376		13.21	7.0E-33	AW671307.1	EST_HUMAN	EST383398 IMAGE resequences, MAGI Homo sapiens cDNA
3718	8858		1.08	8.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1787	6913		1.49	5.0E-33	BF373515.1	EST_HUMAN	QV1-F10168-100700-271-e02 F10169 Homo sapiens cDNA
1806	7024	12243	2.06	6.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1805	7024	12244	2.06	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
2281	7361		1.73	6.0E-33	AL163285.2	NT	Homo sapiens spermidine synthase (SRM) mRNA
4032	9163	14305	0.86	5.0E-33	AB014598.1	NT	Homo sapiens mRNA for KIAA0639 protein, partial cds
1126	6268		1.89	4.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2117	7232	12474	3.01	4.0E-33	4758987	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2397	7603		2.47	4.0E-33	AA626621.1	EST_HUMAN	ab51b1.r1 Stragene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28.b2 MER28 repetitive element;
2616	7620	12868	1.28	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4482	9651	14719	1.67	4.0E-33	AW293349.1	EST_HUMAN	UHH-B12-ah1-c-03-0-U1.NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1090	6220		4.74	3.0E-33	BE350127.1	EST_HUMAN	h109g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148258 3' similar to contains MER28.b3 MER28 repetitive element;
1091	6228		4.22	3.0E-33	BE350127.1	EST_HUMAN	h109g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148258 3' similar to contains MER28.b3 MER28 repetitive element;
2428	7840		1.24	3.0E-33	AV647651.1	EST_HUMAN	AY647651 GLO Homo sapiens cDNA clone GLC8CF09 3'
18	6227		1.23	2.0E-33	AI160188.1	EST_HUMAN	qb67g03.x1 Scarsa_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFRL1 ORF repetitive element;
101	6227		1.88	2.0E-33	AI160188.1	EST_HUMAN	qb67g03.x1 Scarsa_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFRL1 ORF repetitive element;
4397	9517		3.87	2.0E-33	BE159039.1	EST_HUMAN	MIR0-H10405-160300-202-018 HT0405 Homo sapiens cDNA
4970	10078	15215	15.38	2.0E-33	AA826883.1	EST_HUMAN	ab51g1.1.1 Stralagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gb:200734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
5078	10179	15314	1.37	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5078	10179	15315	1.37	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
8	5219		1.37	1.0E-33	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2151	7264	12512	1.17	8.0E-34	8922761	NT	Homo sapiens hypothetical protein FLJ10800 (FLJ10800), mRNA
4475	9594	14733	0.91	8.0E-34	BE062570.1	EST_HUMAN	QV2-BT02558-071289-019-g07 BT02558 Homo sapiens cDNA
1456	6583	11771	1.63	7.0E-34	U70946.1	EST_HUMAN	YF16905.1 Scarsa fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
470	5637	10778	1.44	6.0E-34	U10891.1	NT	Human G2 protein mRNA, partial cds
470	5637	10779	1.44	6.0E-34	U10891.1	NT	Human G2 protein mRNA, partial cds
1890	7010		2.57	5.0E-34	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
5044	10146	15275	4.3	5.0E-34	U30883.1	NT	Human splicing factor SFR55-1 (SFR55) mRNA, complete cds
6127	10227		1.06	6.0E-34	N6282.1	EST_HUMAN	z227g1.1 Scarsa fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:283828 5'
1899	7116	12352	1.33	4.0E-34	A1804867.1	EST_HUMAN	gb4c08.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2249194 3'
2881	7778	13028	1.69	4.0E-34	8922807	NT	Homo sapiens hypothetical protein FLJ10889 (FLJ10889), mRNA
3152	8303	13468	1.02	4.0E-34	5803168	NT	Homo sapiens splicing factor 3a, subunit 3, 60kD (SF3A3), mRNA
1520	6647	11834	18.47	1.0E-34	P12236	SWISSPROT	ADP ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3651	8760	13944	1.42	1.0E-34	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4045	9178	14317	0.75	1.0E-34	AY008397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4045	9178	14318	0.75	1.0E-34	AY008397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4469	9578		2.13	1.0E-34	BE071414.1	EST_HUMAN	RC2-BT0508-240400-016-H08 BT0508 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4908	10018	15163	1.45	1.0E-34	BF609718.1	EST_HUMAN	UH-B14-epb-h-04-0-U1.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086839 3'
4909	10018	15164	1.45	1.0E-34	BF609718.1	EST_HUMAN	UH-B14-epb-h-04-0-U1.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086839 3'
3823	8762	13918	1.31	9.0E-35	AW683302.1	EST_HUMAN	h777606.y1 NCL CGAP_GUT Homo sapiens cDNA clone IMAGE:2068787 5'
223	5416		39.82	6.0E-35	6031180	NT	Homo sapiens prohibitin (PHB) mRNA
1749	6875	12060	2.13	8.0E-35	BF689337.1	EST_HUMAN	nas3a08.x1 NCL CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:075912
1749	6875	12081	2.13	8.0E-35	BF689337.1	EST_HUMAN	nas3a08.x1 NCL CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:075912
4836	9948	15082	2.74	8.0E-35	BF183195.1	EST_HUMAN	075912 DIACYLGLYCEROL KINASE IOTA ;
1420	6547	11728	0.98	8.0E-35	AA167115.1	EST_HUMAN	601809588F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040324 6'
1970	7087	12314	5.54	6.0E-35	6005875	NT	af63403.s1 Soares_testis_NHT Homo sapiens cDNA clone 1305397 3'
4021	9158	14301	0.86	8.0E-35	AW297191.1	EST_HUMAN	Homo sapiens zinc finger protein 208 (ZNF208), mRNA
1724	6851	12055	1.38	5.0E-35	X633392.1	NT	UH-BW0-ajd-4-08-0-U1.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2731433 3'
2745	7839	13084	1.34	8.0E-35	AB007656.2	NT	H sapiens immunoglobulin kappa light chain variable region L14
2880	8135	13288	1.38	6.0E-35	6912638	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
4387	8507	14649	1.91	6.0E-35	AF023268.1	NT	Homo sapiens cdk2 kinase (CLK2), protein1, cat1, glucocorticoidase (GBA), and metadn genes, complete cds; metadn pseudogene and glucocorticoidase pseudogene; and thrombospondin3 (THBS3) gene, partial cds
1444	6572	11769	28.26	4.0E-35	BE267607.1	EST_HUMAN	601109719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 6'
1830	6953	12174	6.38	4.0E-35	H91193.1	EST_HUMAN	yue8a07.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:241238 5' similar to contlns PTR5 repetitive element;
1592	6721	11911	40.86	3.0E-35	BE268182.1	EST_HUMAN	601125260F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 6'
2312	7421		1.77	3.0E-35	AF224492.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
104	7883	10450	1.28	2.0E-35	N88935.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
1190	8324	11492	1.28	2.0E-35	T11909.1	EST_HUMAN	A971F Heart Homo sapiens cDNA clone A971
2200	7312	12564	2.32	2.0E-35	AB018413.1	NT	Homo sapiens mRNA for Gab2, complete cds
2845	7743	12886	1.9	2.0E-35	AW665005.1	EST_HUMAN	h88a12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2879166 3' similar to
3293	8440	13601	0.62	2.0E-35	6912459	NT	SW:TR12_HUMAN Q14669 THYROID RECEPTOR INTERACTING PROTEIN 12;
3293	8440	13602	0.62	2.0E-35	6912459	NT	Homo sapiens Gb2-associated binder 2 (KIAA0571), mRNA
3543	8694		1.04	2.0E-35	AB020702.1	NT	Homo sapiens Gb2-associated binder 2 (KIAA0571), mRNA
3887	9023	14180	0.77	2.0E-35	BE247676.1	EST_HUMAN	Homo sapiens mRNA for KIAA0895 protein, partial cds
							TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TOBAP4328

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3887	9023	14181	0.77	2.0E-35	BE247573.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Bay/et-HQSC project-TCBA Homo sapiens cDNA clone TCBAP4328
4840	8755		2.94	2.0E-35	H49239.1	EST_HUMAN	Y18812.1 Sources fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:274078 5'
45	5257	10378	4.38	1.0E-35	AA631049.1	EST_HUMAN	Inf118 Regional genome DNA specific cDNA library Homo sapiens cDNA clone CR12-1
45	5257	10379	4.38	1.0E-35	AA631949.1	EST_HUMAN	Inf118 Regional genome DNA specific cDNA library Homo sapiens cDNA clone CR12-1
751	5907	11082	16.62	1.0E-35	AW388473.1	EST_HUMAN	IL2-ST0162-131099-008-d12 ST0162 Homo sapiens cDNA
751	5907	11083	16.62	1.0E-35	AW388473.1	EST_HUMAN	IL2-ST0162-131099-008-d12 ST0162 Homo sapiens cDNA
910	6060		1.46	1.0E-35	T87947.1	EST_HUMAN	Y493d01.1 Sources fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:115762 5' similar to SP-A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN;
2513	7616	12863	3.28	1.0E-35	7706994	NT	Homo sapiens hypodermal protein (LOC81233), mRNA
2728	7824	13079	1.24	1.0E-35	BE350127.1	EST_HUMAN	MER29 repetitive element;
2728	7824	13080	1.24	1.0E-35	BE350127.1	EST_HUMAN	MER29 repetitive element;
3121	8273	13429	1.25	1.0E-35	6008030	NT	Homo sapiens transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L), mRNA
3142	8283	13460	3.15	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLOCER08 3'
3142	8283	13451	3.15	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLOCER08 3'
4400	8520	14680	3.82	1.0E-35	7866905	NT	Mus musculus actin receptor interacting protein 1 (Arip1-pending), mRNA
4400	8520	14681	3.82	1.0E-35	7866905	NT	Mus musculus actin receptor interacting protein 1 (Arip1-pending), mRNA
3960	8095	14247	0.96	9.0E-38	AW821707.1	EST_HUMAN	RC3-ST0315-180200-013-f12 ST0315 Homo sapiens cDNA
2896	8050	13217	1.52	7.0E-36	AW657679.1	EST_HUMAN	CMT1-CT0315-091298-089-d07 CT0315 Homo sapiens cDNA
3094	8247		4.75	7.0E-36	4557498	NT	Homo sapiens C-terminal binding protein 2 (CTBP2), mRNA
2005	7122	12358	1.48	6.0E-36	7706622	NT	Homo sapiens nirpinin 2 (NINJ2), mRNA
2395	7501		4	6.0E-36	AB036346.1	NT	Homo sapiens TCEB gene, exon 12
3617	8766	13912	0.81	6.0E-36	BF515101.1	EST_HUMAN	U1-HBW1-ant-c-12-Q-U1e1 NCL CGAP Sub7 Homo sapiens cDNA clone IMAGE:3083642 3'
4943	10053	15191	1.26	6.0E-36	AB030507.1	NT	Rattus norvegicus mRNA for DLG8 gamma, complete cds
139	5331	10476	11.17	5.0E-36	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2714	7809	13063	62.37	5.0E-36	BE388438.1	EST_HUMAN	601285567F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5'
3596	8735	13937	1.6	5.0E-36	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4755	9858	15017	1.95	6.0E-36	5729729	NT	Homo sapiens API6-like 1 (API6L1), mRNA
4755	9858	15018	1.95	6.0E-36	5729729	NT	Homo sapiens API6-like 1 (API6L1), mRNA
1227	6359	11529	2.69	4.0E-36	BE010038.1	EST_HUMAN	PM3-BN0178-100400-001-q04 BN0178 Homo sapiens cDNA
1453	6580	11769	1.93	4.0E-36	P10266	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1657	6786	11979	1.72	4.0E-36	BE382574.1	EST_HUMAN	601288574F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628388 5'
2204	7316		5.27	4.0E-36	AW247772.1	EST_HUMAN	2820020.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
3335	8481	13047	1.86	4.0E-36	BE369289.1	EST_HUMAN	601282289F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
3335	8481	13848	1.86	4.0E-36	BE369289.1	EST_HUMAN	601282289F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
4719	9833	14977	0.63	4.0E-36	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C304
5110	10211	15349	0.74	4.0E-36	AA905361.1	EST_HUMAN	ck05b11.at Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1508809 3' similar to SW:D8HL_RAT P29288 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
694	5851	10998	2.84	3.0E-36	AF089810.1	NT	Homo sapiens neuraxin III-alpha gene, partial cds
1512	6838	11828	1.43	3.0E-36	AF110239.1	NT	Homo sapiens calcitriol/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
1612	6839	11827	1.43	3.0E-36	AF110239.1	NT	Homo sapiens calcitriol/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
2273	7383	12631	1.23	3.0E-36	7682401	NT	Homo sapiens KIAA0962 protein (KIAA0962), mRNA
4479	9589	14738	7.19	3.0E-36	10181139	NT	Mus musculus junctophilin 1 (Jp1-pending), mRNA
3149	8300	13460	5.87	2.0E-36	BE269287.1	EST_HUMAN	601108343F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3342708 5'
4939	10049	15187	8.66	2.0E-36	AW880378.1	EST_HUMAN	QVQ-OT0030-240300-174-H04 OT0030 Homo sapiens cDNA
888	6036	11207	1.87	1.0E-36	BE408310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2126	7243	12486	1.08	1.0E-36	BE146623.1	EST_HUMAN	RC1-HT0217-131168-021-H07 HT0217 Homo sapiens cDNA
2126	7243	12487	1.08	1.0E-36	BE146623.1	EST_HUMAN	RC1-HT0217-131168-021-H07 HT0217 Homo sapiens cDNA
2185	7288	12546	1.32	1.0E-36	BF973761.1	EST_HUMAN	602138493F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272888 5'
3826	8473		1.34	1.0E-36	AF168882.1	NT	Homo sapiens human endogenous retrovirus W prov8-19 protease (pro) gene, partial cds
1288	6417		3.18	7.0E-37	AL042800.1	EST_HUMAN	DKFZP434E0422_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZP434E0422 5'
1756	6882	12088	0.85	7.0E-37	AF111187.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
1756	6882	12089	0.85	7.0E-37	AF111187.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
2401	7607	12758	2.5	4.0E-37	AA102794.1	EST_HUMAN	2890004.61 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
2012	7128	12366	1.98	3.0E-37	AL048856.1	EST_HUMAN	DKFZP434L2418_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZP434L2418
2012	7128	12367	1.98	3.0E-37	AL048856.1	EST_HUMAN	DKFZP434L2418_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZP434L2418
2463	7587		4.6	3.0E-37	AW931150.1	EST_HUMAN	EST1373222 IMAGE resequences, MAGF Homo sapiens cDNA
2834	8088		3.51	3.0E-37	AW931150.1	EST_HUMAN	EST1373222 IMAGE resequences, MAGF Homo sapiens cDNA
379	5588	10733	1.65	2.0E-37	D89790.1	NT	Homo sapiens mRNA for AML1, complete cds
379	5588	10734	1.65	2.0E-37	D89790.1	NT	Homo sapiens mRNA for AML1, complete cds
1082	6221	11397	2.12	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002168 5'

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1082	8221	11388	2.12	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002186 5'
3870	8008	14162	5.62	2.0E-37	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
4224	8849	14482	0.88	2.0E-37	4826885	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
2081	7197	12442	3.65	1.0E-37	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
3180	8331		1.18	1.0E-37	AW882882.1	EST_HUMAN	RC3-CT0347-210400-016-H03 CT0347 Homo sapiens cDNA
3834	8070	14226	0.78	1.0E-37	AF189011.1	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
4918	10028	15170	2.24	1.0E-37	BF371719.1	EST_HUMAN	QV0-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
1224	6956	11626	1.79	8.0E-38	11436955	NT	Homo sapiens Grb2-associated binder 2 (GAB2), mRNA
2469	7573	12826	1.23	8.0E-38	BF346221.1	EST_HUMAN	802018401F1 NCL_OCAP_Bim87 Homo sapiens cDNA clone IMAGE:4163892 5'
2165	7278	12525	3.81	7.0E-38	AW872825.1	EST_HUMAN	EST384920 MAGE sequences, MAGL Homo sapiens cDNA
3073	8226	13377	1.1	7.0E-38	AW884259.1	EST_HUMAN	QV3-OT0084-060400-144-f08 OT0084 Homo sapiens cDNA
4200	8426	14466	0.82	7.0E-38	H16092.1	EST_HUMAN	Yr57167.1 Scores adult brain N26541B55Y Homo sapiens cDNA clone IMAGE:171673 5'
3014	8168	13328	1.89	6.0E-38	BF63093.1	EST_HUMAN	601456722F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3858348 5'
725	5881	11028	1.5	5.0E-38	AW871818.1	EST_HUMAN	EST383308 MAGE sequences, MAGL Homo sapiens cDNA
2430	7634	12787	3.2	5.0E-38	AJ237740.1	NT	Homo sapiens RIBIR gene (partial), exon 8
115	5317	10458	3.02	4.0E-38	Z25488.1	NT	B. taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
1159	6295	11460	0.88	3.0E-38	11435847	NT	B. taurus mitochondrial aspartate aminotransferase mRNA, complete CDS
2091	7206		2.18	3.0E-38	AF003530.1	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
3673	8812		1.76	3.0E-38	7549807	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3834	8970	14125	1.48	3.0E-38	P63638	SWISSPROT	Homo sapiens HIRA interacting protein 4 (dnad-like) (HIRAP4), mRNA
49	5281	10386	1.61	2.0E-38	AL163248.2	SWISSPROT	SSU72 PROTEIN
1390	6518	11858	6.25	2.0E-38	5802087	NT	Homo sapiens chromosome 21 segment HS21C048
1658	6786	11880	1.88	2.0E-38	AA437553.1	EST_HUMAN	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
1658	6786	11881	1.88	2.0E-38	AA437553.1	EST_HUMAN	zw30d01.1 Scores ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:770788 5' similar to
3520	8681		1.04	2.0E-38	AF070670.1	NT	SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
4534	8872	14814	14.66	2.0E-38	4557887	NT	zw30d01.1 Scores ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:770788 5' similar to
1094	8232		1.83	1.0E-38	AA401670.1	EST_HUMAN	SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
2000	7117	12353	1.95	1.0E-38	4885298	NT	Homo sapiens protein phosphatase 2C alpha 2 mRNA, complete cds
							Homo sapiens keratin 18 (KRT18) mRNA
							zw30d02.1 Scores testis_NHT1 Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element
							MER18 repetitive element ;
							Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA

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Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2016	7132	12369	1.02	1.0E-39	7661889	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
2468	7670	12824	3.73	1.0E-39	AF270831.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
4127	8235	14394	1.03	1.0E-39	AB037863.1	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4301	9423	14556	1.44	1.0E-39	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4301	9423	14557	1.44	1.0E-39	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4670	8888	14826	1.07	1.0E-39	8922343	NT	Homo sapiens hypothetical protein FLJ10800, mRNA
53	5265	10392	3.67	8.0E-39	4602312	NT	Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA
1401	6528	11708	1.7	8.0E-39	4758229	NT	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
1843	8884		1.85	8.0E-39	AI823404.1	EST_HUMAN	wt53110.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384481 3' similar to TRP87880 P87880
2085	7201	12445	3.54	7.0E-39	AL163227.2	NT	POL PROTEIN:
1008	6152	11319	2.47	5.0E-39	AF003528.1	NT	Homo sapiens chromosome 21 segment HS21C027
2554	8108	13272	0.8	5.0E-39	AI750154.1	EST_HUMAN	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
549	5714	10948	28.8	4.0E-39	AB015810.1	NT	cd38b04.x1 Bortezomib cdon HPLR87 Homo sapiens cDNA clone IMAGE:2374083 3' similar to TR-Q15408
3559	8700	13660	0.71	4.0E-39	AL163210.2	NT	Q15-408 NEUTRAL PROTEASE LARGE SUBUNIT: contains LTR7.11 LTR7 repetitive element;
46	6268	10380	12.67	3.0E-39	AA631949.1	EST_HUMAN	Gliorobus satipops mRNA for ribosomal protein S4X, complete cds
46	5258	10381	12.67	3.0E-39	AA631949.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
46	5258	10382	12.67	3.0E-39	AA631949.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
808	6048		7.83	2.0E-39	BE405203.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
813	6063		11.41	2.0E-39	AI525119.1	EST_HUMAN	fmfc16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
1033	8174		3.5	2.0E-39	AF000573.1	NT	601301607FT NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'
1544	6872		60.74	2.0E-39	AW372318.1	EST_HUMAN	promtr-7.D01.1 bifurcator Homo sapiens cDNA 5'
1978	7092	12322	1.87	2.0E-39	AA720574.1	EST_HUMAN	Homo sapiens homogenitase 1,2-dioxygenase gene, complete cds
2594	7696	12949	1.06	2.0E-39	AL163248.2	NT	PM0-BT0340-211289-003-402 BT0340 Homo sapiens cDNA
4382	8563	14846	1.98	2.0E-39	BF370207.1	EST_HUMAN	nv21g02.e1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.3
1528	6855	11842	2.69	1.0E-39	AJ008345.1	NT	THR repetitive element:
1528	6855	11843	2.69	1.0E-39	AJ008345.1	NT	Homo sapiens chromosome 21 segment HS21C048
1545	6873	11857	3.43	1.0E-39	AW651985.1	EST_HUMAN	RC4-FN0037-290700-011-a10 FN0037 Homo sapiens cDNA
4630	9748	14893	12.37	1.0E-39	AW651985.1	EST_HUMAN	Homo sapiens KVLQ11 gene
4630	9748	14894	12.37	1.0E-39	AW651985.1	EST_HUMAN	Homo sapiens KVLQ11 gene

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Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4671	9787	14832	7.78	1.0E-39	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
664	5718	10851	1.73	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1238	6368	11640	8.31	9.0E-40	4765145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1238	6368	11641	8.31	9.0E-40	4765145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1482	6589	11778	1.72	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
3764	8901	14053	0.79	9.0E-40	4503764	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
3946	10307	14233	3.8	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
3013	8167	13325	0.97	8.0E-40	AA078165.1	EST_HUMAN	7H15A04 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H15A04
3897	9033		4.43	8.0E-40	BE395641.1	EST_HUMAN	60128858F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3618168 5'
2888	7788	13035	7.39	8.0E-40	AA381275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to similar to zinc finger protein family
2689	7788	13038	7.39	8.0E-40	AA381275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to similar to zinc finger protein family
2669	7670	12925	1.21	6.0E-40	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1887	7007	12227	1.7	4.0E-40	AI688006.1	EST_HUMAN	181501.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:O73505 O73505 POL PROTEIN ;
2089	7214		2.31	4.0E-40	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4397	9488	14832	8.7	4.0E-40	7682117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
4103	9232	14369	0.8	3.0E-40	AI925949.1	EST_HUMAN	wh1207.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2380548 3'
323	6508		5.15	2.0E-40	AI223038.1	EST_HUMAN	gg32h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838847 3'
795	5948		20.8	2.0E-40	AW303888.1	EST_HUMAN	xr24a10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2781088 3' similar to SW:RSS_MOUSE
1838	6959		1.06	2.0E-40	AV731601.1	EST_HUMAN	P97461 40S RIBOSOMAL PROTEIN S6 ;
1838	7067	12278	4.87	2.0E-40	4506188	NT	AV731601 HTF Homo sapiens cDNA clone HTFAZE05 5'
1838	7067	12278	4.87	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2150	7283	12511	1.98	2.0E-40	5453592	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2851	7749		1.88	2.0E-40	BE27632.1	EST_HUMAN	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
3103	8256	13407	4.43	2.0E-40	5453592	NT	601121587F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5'
4874	8985	15132	1.41	2.0E-40	AL163280.2	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
4874	8985	15133	1.41	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
884	6334		26.04	1.0E-40	AA225689.1	EST_HUMAN	ncd9e09.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007608
2588	7687	12942	5.11	1.0E-40	BF030881.1	EST_HUMAN	601480375F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3863803 5'
2647	7745		1.35	1.0E-40	BE018348.1	EST_HUMAN	b578a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q8Z168 Q8Z168
2689	7785	13045	1.07	1.0E-40	BF641030.1	EST_HUMAN	SYNTAXIN 17.
2699	7795	13046	1.07	1.0E-40	BF641030.1	EST_HUMAN	602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4087738 5'
3280	8429		1.29	1.0E-40	4507142	NT	602068604F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4087738 5'
4592	9700	14838	8.49	1.0E-40	4508012	NT	Homo sapiens sorting nexin 3 (SNX3) mRNA
3782	8919	14070	0.6	9.0E-41	W01598.1	EST_HUMAN	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
829	7802	11148	1.72	7.0E-41	AB34384.1	EST_HUMAN	zab36a02.r1 Soares fetal liver spleen 1NF1LS Homo sapiens cDNA clone IMAGE:294602 5'
4827	9745	14889	1.16	7.0E-41	AB34384.1	EST_HUMAN	wp04h104.x1 NCI_CGAP_K6111 Homo sapiens cDNA clone IMAGE:2463895 3'
4827	9745	14889	1.16	7.0E-41	BE388592.1	EST_HUMAN	wp04h104.x1 NCI_CGAP_K6111 Homo sapiens cDNA clone IMAGE:2463895 3'
278	5467	10610	2.24	8.0E-41	AB037163.1	NT	601282077F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3803965 5'
2101	7218	12463	1.5	6.0E-41	7657042	NT	601282077F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3803965 5'
1814	6337	12153	1.12	5.0E-41	T62828.1	EST_HUMAN	Homo sapiens DSCR5b mRNA, complete cds
4083	9212		1.07	5.0E-41	4885636	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
398	5568		1.74	4.0E-41	BE195318.1	EST_HUMAN	yc03af10.s1 Stratiopsis lung (#937210) Homo sapiens cDNA clone IMAGE:79628 3'
1099	8237	11400	1.28	4.0E-41	AU118344.1	EST_HUMAN	Homo sapiens target of myb1 (chicken) homolog (TOM1), mRNA
							QV0-HT0367-150200-114-q09 HT0367 Homo sapiens cDNA
							AU118344 HEMBA1 Homo sapiens cDNA clone HEMBA1005683 5'
1417	6544	11723	8.1	4.0E-41	AI027117.1	EST_HUMAN	qw45e06.s1 Soares_papillary_thyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649784 3' similar to TR:Q00897 Q00897 CYTOCHROME C-LIKE POLYPEPTIDE, contains LTR5.b1 LTR6 repetitive element;
1417	6544	11724	8.1	4.0E-41	AI027117.1	EST_HUMAN	qw45e06.s1 Soares_papillary_thyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649784 3' similar to TR:Q00897 Q00897 CYTOCHROME C-LIKE POLYPEPTIDE, contains LTR5.b1 LTR6 repetitive element;
1432	6569	11742	1.48	4.0E-41	AB008681.1	NT	TR:Q00897 Q00897 CYTOCHROME C-LIKE POLYPEPTIDE, contains LTR5.b1 LTR6 repetitive element;
1648	6774	11866	4.24	4.0E-41	AI500408.1	EST_HUMAN	qw45e06.s1 Soares_papillary_thyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649784 3' similar to TR:Q00897 Q00897 CYTOCHROME C-LIKE POLYPEPTIDE, contains LTR5.b1 LTR6 repetitive element;
2856	8010	13171	3.4	4.0E-41	AJ228041.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
2856	8010	13172	3.4	4.0E-41	AJ228041.1	NT	fm9e04.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1 OFR repetitive element;
4115	9243	14378	1.67	4.0E-41	X92685.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
948	6096	11264	1.63	3.0E-41	AB030176.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4311	9433	14568	2.53	3.0E-41	AB026898.1	NT	H. sapiens DNase I hypersensitive site (HSS-3) enhancer element
							Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5090	10190		1.14	3.0E-41	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1837	6704	11894	30.23	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
1992	7079	12303	1.48	2.0E-41	AA331940.1	EST_HUMAN	EST135918 Embryo, 8 week 1 Homo sapiens cDNA 5' end
2201	7313	12565	2.00	2.0E-41	D88932.1	NT	Human mRNA for KIAA0207 gene, complete cds
2248	7358	12615	6.13	2.0E-41	X98931.1	NT	G. gorilla DNA for ZNF80 gene homolog
2768	8704	11894	12.66	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
3815	8952	14100	0.81	2.0E-41	5032108	NT	Homo sapiens son of sevenless (Drosophila) homolog 1 (SOS1) mRNA
4691	9709	14847	1.07	2.0E-41	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4591	9709	14848	1.07	2.0E-41	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
3180	8341	13503	1.08	1.0E-41	BE889735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
3180	8341	13504	1.08	1.0E-41	BE889735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
4539	9657	14801	12.01	1.0E-41	6878488	NT	Mus musculus tubulin alpha 6 (Tub6), mRNA
482	5630	10769	4.87	8.0E-42	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
5131	10231	15368	0.67	8.0E-42	6879031	NT	Mus musculus neural precursor cell expressed, developmentally down-regulated gene 1 (Nedd1), mRNA
933	6081		2.26	7.0E-42	AL163286.2	NT	Homo sapiens chromosome 21 segment HS21C085
1887	6987	12209	2.26	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
1887	6987	12210	2.26	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2268	7378		1.62	6.0E-42	AW238659.1	EST_HUMAN	xc29f08.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741789 3' similar to contains L1.L1 L1 repetitive element
4991	10097						qu24h09.x1 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1985761 similar to contains Alu repetitive element
131	6329		1.61	6.0E-42	A1284770.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 1/2
437	6608	10760	5.3	5.0E-42	AJ271735.1	NT	h31e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
488	5654		4.28	5.0E-42	BE217913.1	EST_HUMAN	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
487	5655		2.43	6.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
762	5908	11064	2.41	4.0E-42	AF055086.1	NT	Homo sapiens MHC class 1 region
752	5908	11065	2.41	4.0E-42	AF055086.1	NT	Homo sapiens MHC class 1 region
1087	6207	11370	2.48	4.0E-42	AF180111.1	NT	Homo sapiens ribonuclease III (RNI3) mRNA, complete cds
4198	9292	14430	1.58	4.0E-42	X69417.1	NT	H. sapiens PROS-27 mRNA
4205	9300	14463	0.97	4.0E-42	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4227	9352	14485	4.48	4.0E-42	4508496	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA
4657	9678	14818	11.81	4.0E-42	4508008	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
1493	6820	11810	1.64	2.0E-42	BF378834.1	EST_HUMAN	RC0-TN0078-110900-024-g07 TN0078 Homo sapiens cDNA

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Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2389	7495		2.18	2.0E-42	AW898344.1	EST_HUMAN	RC3-NIN0070-270400-011-h10 NN0070 Homo sapiens cDNA
2402	7508	12767	13.89	2.0E-42	AW260059.1	EST_HUMAN	2819293.3 prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819293.3'
732	5887	11039	2.53	1.0E-42	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV6)
1044	6185	11382	0.89	1.0E-42	AW288809.1	EST_HUMAN	U1-H-B1-afh-e-04-Q-JL.s1 NCL_CGAP_Sub33 Homo sapiens cDNA clone IMAGE:2721871.3'
1102	6240	11403	1.05	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1102	6240	11404	1.05	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1248	7912	11654	10.38	1.0E-42	AF067168.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AQQG subunit precursor homodog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1248	7912	11655	10.38	1.0E-42	AF067168.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AQQG subunit precursor homodog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1715	6842	12045	0.95	1.0E-42	11423219	NT	Homo sapiens rec (LOC61201), mRNA
2025	7142	12382	1.17	1.0E-42	AF110298.1	NT	Homo sapiens PDNP1 gene, exon 17
2615	7619	12887	1.01	1.0E-42	6174468	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
2633	8087	13254	5.88	1.0E-42	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
3086	8825	13980	2.3	1.0E-42	7682027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3772	8909	14082	0.83	1.0E-42	5031610	NT	Homo sapiens Gdgi vesicular membrane trafficking protein p18 (BET1) mRNA
3800	9038	14186	1.09	1.0E-42	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4225	9350	14483	1.87	1.0E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4366	9684	14823	0.89	1.0E-42	AW813817.1	EST_HUMAN	RC3-ST0187-161089-012-e03 ST0187 Homo sapiens cDNA
4711	9827	14970	2.01	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (P31), mRNA
4711	9827	14971	2.01	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (P31), mRNA
4748	9859	15008	4.99	1.0E-42	4508758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4942	9854	16099	1.01	1.0E-42	AB03114.1	NT	Homo sapiens mRNA for KIAA1288 protein, partial cds
651	5812	10947	18.09	8.0E-43	AV736824.1	EST_HUMAN	AV736824 C8 Homo sapiens cDNA clone CBLAKH08.5'
651	5812	10948	18.09	8.0E-43	AV736824.1	EST_HUMAN	AV736824 C8 Homo sapiens cDNA clone CBLAKH08.6'
688	5855	11000	5.14	8.0E-43	8823276	NT	Homo sapiens hypothetical protein FLJ20287 (FLJ20287), mRNA
688	5855	11001	5.14	8.0E-43	8823276	NT	Homo sapiens hypothetical protein FLJ20287 (FLJ20287), mRNA
688	5855	11002	5.14	8.0E-43	8823276	NT	Homo sapiens hypothetical protein FLJ20287 (FLJ20287), mRNA
3918	6758	13914	6.42	7.0E-43	AW246442.1	EST_HUMAN	2822251.3 prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251.5'
1349	6478		32.87	6.0E-43	AA491890.1	EST_HUMAN	nt/24006.81 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:809803 similar to gbtL05095.60S
2654	7657		2.04	6.0E-43	AV708201.1	EST_HUMAN	RIBOSOMAL PROTEIN L30 (HUMAN)
138	5335		1.73	6.0E-43	AL163213.2	NT	AV708201 ADC Homo sapiens cDNA clone ADGACC10.5'
						NT	Homo sapiens chromosome 21 segment HS21C013

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
502	5659	10803	2.55	5.0E-43	AA382780.1	EST_HUMAN	ESTB0033 Testis 1 Homo sapiens cDNA 5' end
2809	7065	13126	1.81	5.0E-43	AV732578.1	EST_HUMAN	AV732578 HITF Homo sapiens cDNA clone HTFANC08.5
974	7887	11260	12.54	4.0E-43	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1216	6348		3.61	3.0E-43	AF223301.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1708	5836	12037	4.39	3.0E-43	X97859.1	NT	H. sapiens gene encoding La autoantigen
3558	8699	13859	1.14	3.0E-43	S96002.1	NT	AML1-EV1-1-AML1-EV1-1 fusion protein (rearranged translocation) [human, leukemic cell line SICH1, mRNA Mutant, 5938 nt]
4266	8391	14629	0.77	3.0E-43	AA548154.1	EST_HUMAN	hM55d08.at NCI_CGAP_P7 Homo sapiens cDNA clone IMAGE:1017418
179	5373		0.84	2.0E-43	AI180764.1	EST_HUMAN	q061c09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733968 3' similar to contains PTR7.13
1692	8760	11085	2.83	1.0E-43	AF154836.1	NT	PTR7 PTR7 repetitive element 1
1802	8760	11908	2.83	1.0E-43	AF154836.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1720	6847	12051	1.05	1.0E-43	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2898	7763	13031	5.01	1.0E-43	BF348283.1	EST_HUMAN	602022313F1 NCI_CGAP_Bim87 Homo sapiens cDNA clone IMAGE:4167688 5'
891	6041	11212	4.32	8.0E-44	AI222885.1	EST_HUMAN	q023g01.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
891	6041	11213	4.32	8.0E-44	AI222885.1	EST_HUMAN	q023g01.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
4843	8855	15100	1.08	8.0E-44	AW373185.1	EST_HUMAN	RCS-BT0503-081268-011-g12 BT0503 Homo sapiens cDNA
4843	8855	15101	1.08	8.0E-44	AW373185.1	EST_HUMAN	RCS-BT0503-081268-011-g12 BT0503 Homo sapiens cDNA
658	5819		1.87	7.0E-44	R08035.1	EST_HUMAN	y689d01.J1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:124920 5'
2215	7327	12579	1.12	7.0E-44	S031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
2835	8089	13255	2.28	7.0E-44	AF048726.1	NT	Homo sapiens minisatellite ms32 repeat region
2836	8089	13256	2.28	7.0E-44	AF048726.1	NT	Homo sapiens minisatellite ms32 repeat region
3841	8977	14132	2.47	7.0E-44	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4220	8346	14476	0.89	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4220	8346	14477	0.89	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
5107	10208	15345	0.81	7.0E-44	AF111188.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
301	5489		3.01	5.0E-44	AJ283880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
330	5513		2.52	5.0E-44	AJ283880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
3306	8540	13689	3.05	4.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
5002	10107		1.11	4.0E-44	AI435225.1	EST_HUMAN	111d02.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
1786	8921		1.25	3.0E-44	6912477	NT	Homo sapiens karyopherin alpha 6 (importin alpha 7) (KPNA6), mRNA
2503	7606	12856	2.91	3.0E-44	BE880626.1	EST_HUMAN	601481629F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3883839 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3071	8224	13375	5.78	3.0E-44	AA168851.1	EST_HUMAN	z18b05.r1 Stragene fetal retina 837202 Homo sapiens cDNA clone IMAGE:809777 5'
3897	9003	14161	1.29	3.0E-44	AA337234.1	EST_HUMAN	EST42289 Endometrial tumor Homo sapiens cDNA 5' end similar to similar to alpha-1-antitrypsinase F
1051	6182	11356	2.86	2.0E-44	4826685	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp) box polypeptide 1 (DDX1) mRNA
1051	6192	11357	2.96	2.0E-44	4826886	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp) box polypeptide 1 (DDX1) mRNA
1210	6342	11612	5.87	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1210	6342	11613	5.87	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1316	6445	11624	4.08	2.0E-44	AF133688.1	NT	Homo sapiens RAB38 (RAB38) mRNA, complete cds
1378	6508	11687	1.42	2.0E-44	BE46325.1	EST_HUMAN	hw14g08.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3182838 3' similar to SW:OXYB_HUMAN
2136	7250	12498	4.42	2.0E-44	AF070651.1	NT	P22059 OXYSTEROL-BINDING PROTEIN, ;
2574	7674	12498	5.82	2.0E-44	5901833	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
3452	8594	13768	1.59	2.0E-44	D87675.1	NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
4542	8660	14803	1.43	2.0E-44	AW864978.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
61	6263	10389	8.45	1.0E-44	7657334	NT	PIMA-SN0018-120500-003-c04 SN0018 Homo sapiens cDNA
51	5263	10390	8.45	1.0E-44	7657334	NT	Homo sapiens MissheperNIK-related kinase (MINK), mRNA
678	5741	10869	2.85	1.0E-44	AW853132.1	EST_HUMAN	Homo sapiens MissheperNIK-related kinase (MINK), mRNA
1200	8333	10869	1.5	1.0E-44	AW864803.1	EST_HUMAN	RC1-CT0249-030300-028-h12 CT0249 Homo sapiens cDNA
1696	8716		6.07	1.0E-44	AL163303.2	NT	RC1-BN0039-110300-012-401 BN0039 Homo sapiens cDNA
2206	7318	12568	2.63	1.0E-44	AA434554.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
2206	7318	12569	2.63	1.0E-44	AA434554.1	EST_HUMAN	z183d02.L1 Scores_t04_fetus_Nb2HF9_Sw Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.L3 THR repetitive element ;
2722	7817	13073	1.32	1.0E-44	AF189778.1	NT	z183d02.L1 Scores_t04_fetus_Nb2HF9_Sw Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR.L3 THR repetitive element ;
3706	8844		4.58	1.0E-44	AA434554.1	EST_HUMAN	Homo sapiens transcription factor GCM enhancer 3, JM11 protein, JM4 protein, JM5 protein, TS4 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophycin genes, complete cds; and L-type calcium channel alpha
8089	10189	15333	0.9	1.0E-44	AF189778.1	NT	z183d02.L1 Scores_t04_fetus_Nb2HF9_Sw Homo sapiens cDNA clone IMAGE:811884 3'
6095	10189	15334	0.8	1.0E-44	AJ130755.1	NT	z183d02.L1 Scores_t04_fetus_Nb2HF9_Sw Homo sapiens cDNA clone IMAGE:811884 3'
4551	9669	14811	1.98	9.0E-45	8922391	NT	Homo sapiens alpha satellite DNA, M1 monomer type
4551	9669	14812	1.98	9.0E-45	8922391	NT	Homo sapiens alpha satellite DNA, M1 monomer type
2486	7800	12848	6.36	8.0E-45	5174718	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
5066	10168	15302	7.57	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
2925	8078		1.04	7.0E-45	AL160131.1	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
						NT	Novel human gene mapping to chromosome 22

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3951	8086		6.84	6.0E-45	AW157670.1	EST_HUMAN	au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782908 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
893	8043		2.88	5.0E-45	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2003	7120	12366	2.28	8.0E-46	BF333827.1	EST_HUMAN	CM4-CN0044-180200-615-701 CN0044 Homo sapiens cDNA
3194	8345	13509	2.36	6.0E-45	AI523766.1	EST_HUMAN	ig94h07.x1 NCL CGAP_OLL1 Homo sapiens cDNA clone IMAGE:2118453 3' similar to SW:PAX1_MOUSE P09084 PAIRED BOX PROTEIN PAX-1 ;
1146	8281	11446	8.31	4.0E-45	X95826.1	NT	H.sapiens ART4 gene
2288	7378	12827	3.65	4.0E-45	BE261622.1	EST_HUMAN	601194440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 6'
3312	8468		1.03	3.0E-45	T71480.1	EST_HUMAN	yc35i07.r1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:110245 6'
4084	8459		1.3	3.0E-45	T71480.1	EST_HUMAN	yc35i07.r1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:110245 6'
2472	7678		1.46	2.0E-45	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
3004	8158	13315	1.89	2.0E-45	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
119	5578		1.71	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608183 5'
408	5678		2.78	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608183 5'
472	5839	10781	1.14	1.0E-46	4506412	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
1178	6311	11479	1.44	1.0E-45	7657280	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3078	8232	13383	6.31	1.0E-45	U32189.1	NT	Human pro- $\alpha 2$ chain of collagen type XI (COL11A2) gene, complete cds
3473	8616	13782	0.87	1.0E-45	8659558	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
3560	8701	13861	0.72	1.0E-45	AB046811.1	NT	Homo sapiens mRNA for KIAA1691 protein, partial cds
4456	9575	14714	4.73	1.0E-46	BE389833.1	EST_HUMAN	601280116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619803 5'
2419	7624	12778	25.33	8.0E-48	AI433261.1	EST_HUMAN	832508.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132189 3' similar to gb:J00314_mae2
2419	7624	12777	25.33	8.0E-48	AI433261.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
2220	7332	12585	1.91	7.0E-46	U46007.1	NT	TUBULIN BETA-1 CHAIN (HUMAN);
4653	9871		6.61	7.0E-48	BE386165.1	EST_HUMAN	Rattus norvegicus esph mRNA, complete cds
4775	9888		1.48	7.0E-46	BE084386.1	EST_HUMAN	601277292F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5'
2718	7813	13068	3.3	6.0E-46	AI884381.1	EST_HUMAN	RC4-BT0310-110300-016-f10 BT0310 Homo sapiens cDNA
2718	7813	13069	3.3	6.0E-46	AI884381.1	EST_HUMAN	wn31f08.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2437676 3' similar to contains MER19.12 MER19 repetitive element ;
201	5398		5.07	6.0E-48	AL163210.2	NT	wn31f08.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2437676 3' similar to contains MER19.12 MER19 repetitive element ;
3515	8658	13822	1.28	5.0E-46	BE877194.1	EST_HUMAN	wn31f08.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2437676 3' similar to contains MER19.12 MER19 repetitive element ;
3515	8658	13823	1.28	6.0E-46	BE877194.1	EST_HUMAN	wn31f08.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2437676 3' similar to contains MER19.12 MER19 repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
640	5901		1.91	4.0E-46	AA601143.1	EST_HUMAN	nc54608.s1 NCI_CGAP_S51 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X14008_mai1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1719	6849	12049	8.22	4.0E-46	AW770844.1	EST_HUMAN	h186d03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_mai1 LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element;
1719	6846	12050	8.22	4.0E-46	AW770844.1	EST_HUMAN	h186d03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_mai1 LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element;
2702	7798	13049	1.41	4.0E-46	M18048.1	NT	Human endogenous retrovirus RTVL-H2
5125	10226	15361	0.65	4.0E-46	BE044280.1	EST_HUMAN	h042a07.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040020 3'
5125	10226	15362	0.65	4.0E-46	BE044280.1	EST_HUMAN	h042a07.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040020 3'
2141	7255	12501	2.28	3.0E-46	5453620	NT	Homo sapiens solute carrier family 35 (GNP-staic acid transporter), member 1 (SLC35A1), mRNA
2282	7372	12628	1.87	3.0E-46	7657203	NT	Homo sapiens acidic 82 kDa protein mRNA (HSU75552), mRNA
2406	7512	12762	7.52	3.0E-46	AF160212.1	NT	Homo sapiens VAMP-associated 33 kDa protein mRNA, complete cds
4371	9482	14636	0.81	3.0E-46	4506376	NT	Homo sapiens mitogen-activated protein kinase kinase 3 (MAP4K3), mRNA
4742	9856	15002	1.38	3.0E-46	Z73630.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germ-line; Ig-Lambda; VLambda
4742	9855	15003	1.38	3.0E-46	Z73630.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germ-line; Ig-Lambda; VLambda
839	5990	11158	8.59	2.0E-46	AA468043.1	EST_HUMAN	nc06a09.s1 NCI_CGAP_Oc3 Homo sapiens cDNA clone IMAGE:680408 3' similar to contains THR.B2 THR repetitive element;
1577	6706		1.15	2.0E-46	AA678246.1	EST_HUMAN	z27e11.s1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431866 3'
1652	6780	11972	2.98	2.0E-46	U76027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
4959	10087	15204	1.07	2.0E-46	AA399283.1	EST_HUMAN	z169e02.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:726650 5' similar to SW:RSP1_MOUSE Q01730 RSP-1 PROTEIN;
1236	6386	11639	4.66	1.0E-46	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
2258	7398	12624	2.78	1.0E-46	AW978516.1	EST_HUMAN	EST380825 MAGE resequences, MAGP Homo sapiens cDNA
2377	7463	12737	2.35	1.0E-46	H97330.1	EST_HUMAN	EST484095 WATM1 Homo sapiens cDNA clone 480095
3232	8382	13542	1.72	1.0E-46	AA631912.1	EST_HUMAN	np78602.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:X76717 H. sapiens MT-11 mRNA. (HUMAN);
4844	8956		3.11	1.0E-46	AB023197.1	NT	Homo sapiens mRNA for KIAA0980 protein, partial cds
766	5920		3.32	9.0E-47	AJ271735.1	NT	Homo sapiens Xa pseudautosomal region; segment 1/2

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Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4910	10020	16166	3.19	8.0E-47	AW770928.1	EST_HUMAN	H93604.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3009534 3' similar to TR:O75703 O75703
1820	6943	12167	11.91	8.0E-47	Y18538.1	NT	HYPOTHETICAL 12.4 KD PROTEIN ;
1820	6943	12162	11.91	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 18323
							Homo sapiens HLA-C gene, exon 5, individual 18323
2678	7775	13028	1.41	8.0E-47	6453955	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B58), epsilon isoform (PPP2R5E) mRNA
2686	6167	13312	1.9	8.0E-47	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3606	8746	13900	0.76	8.0E-47	AB041928.1	NT	Homo sapiens HLA-C gene, exon 5, individual 18323
3606	8745	13901	0.75	8.0E-47	AB041928.1	NT	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
2619	7823	12889	1.27	8.0E-47	AL163248.2	NT	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
1407	6534	11713	3.52	4.0E-47	4557598	NT	Homo sapiens chromosome 21 segment HS21C046
643	5709	10844	8.99	3.0E-47	BE907634.1	EST_HUMAN	Homo sapiens E1A binding protein p300 (EP300) mRNA
643	5709	10846	8.69	3.0E-47	BE907634.1	EST_HUMAN	601497839F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3889721 5'
819	5972	11134	3.04	3.0E-47	N57483.1	EST_HUMAN	601497839F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3889721 5'
845	6093	11291	7.87	3.0E-47	AL163284.2	NT	Y64804.s1 Soares multiple sclerosis 2NblMSP Homo sapiens cDNA clone IMAGE:277527 3'
2023	7140	12380	4.73	3.0E-47	AB007889.1	NT	Homo sapiens chromosome 21 segment HS21C084
3285	8434	19598	0.76	3.0E-47	4504116	NT	Homo sapiens KIAA0439 mRNA, partial cds
3039	9076		4.78	3.0E-47	U98181.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4340	9482	14589	1.92	3.0E-47	M12659.1	NT	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
143	8340	10484	1.27	2.0E-47	4908318	NT	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
969	6116	11284	2.44	2.0E-47	AL163209.2	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
969	6116	11285	2.44	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1606	6734	11927	3.51	2.0E-47	7682109	NT	Homo sapiens chromosome 21 segment HS21C009
1691	6820	12019	3.36	2.0E-47	AA524514.1	EST_HUMAN	Homo sapiens KIAA0428 gene product (KIAA0428), mRNA
4324	9446	14579	1.79	2.0E-47	4504868	NT	Homo sapiens C68 Homo sapiens cDNA clone IMAGE:937607 3'
4363	9485	14626	1.84	2.0E-47	AA569592.1	EST_HUMAN	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4363	9485	14627	1.84	2.0E-47	AA569592.1	EST_HUMAN	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4483	9602	14741	1.72	2.0E-47	5174848	NT	m23g07.s1 NCI CGAP P11 Homo sapiens cDNA clone IMAGE:914652
4781	8804	15040	1.14	2.0E-47	AW965186.1	EST_HUMAN	m23g07.s1 NCI CGAP P11 Homo sapiens cDNA clone IMAGE:914652
5181	10276	15416	1.01	2.0E-47	9053268	NT	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R) mRNA
1413	6540	11717	4.29	1.0E-47	A1333429.1	EST_HUMAN	EST377289 MAGC resequences, MAG1 Homo sapiens cDNA
3600	8937	14083	0.98	1.0E-47	BE280477.1	EST_HUMAN	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI), mRNA
3600	8937	14084	0.98	1.0E-47	BE280477.1	EST_HUMAN	q99h03.x1 Soares fetal lung NblL19W Homo sapiens cDNA clone IMAGE:1831189 3'
6059	10161	15294	2.63	1.0E-47	AW813806.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
							601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
							RC3-ST0167-130400-017402 ST0167 Homo sapiens cDNA

Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1625	6753	11946	2.38	9.0E-48	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
1254	6884		1.3	8.0E-48	4501900	NT	Homo sapiens aminocyclase 1 (ACY1), mRNA
1255	6884		1.17	8.0E-48	4501900	NT	Homo sapiens aminocyclase 1 (ACY1), mRNA
3113	8266	13421	3.72	8.0E-48	AW768477.1	EST_HUMAN	h61b03.x1 NCJ CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
3113	8268	13422	3.72	8.0E-48	AW768477.1	EST_HUMAN	h61b03.x1 NCJ CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707 BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
480	5658		1.47	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
481	5658		12.54	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1511	6838	11825	1.42	7.0E-48	6912719	NT	Homo sapiens taurin-like kinase 1 (TLK1), mRNA
1648	6770	11908	5.89	7.0E-48	5730038	NT	Homo sapiens SET domain and nuclear transposase fusion gene (SETMAR) mRNA
3584	8725	13883	0.93	6.0E-48	AI761111.1	EST_HUMAN	w68b03.x1 NCJ CGAP_X612 Homo sapiens cDNA clone IMAGE:2398613 3'
3291	10305	13600	1.62	6.0E-48	4826881	NT	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA
1978	7085	12325	35.4	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
1978	7085	12328	35.4	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
3611	8750	13907	0.7	3.0E-48	AW684531.1	EST_HUMAN	h14b12.x1 NCJ CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872265 3' similar to SW:DCRB_HUMAN
44	5256	10377	2.62	2.0E-48	AA631940.1	EST_HUMAN	P66565 DOWN SYNDROME CRITICAL REGION PROTEIN B. ; hmf77 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR17-28
4506	9625	14768	1.11	2.0E-48	BE246065.1	EST_HUMAN	TCBAP1D3842 Pediatric pro-B cell acute lymphoblastic leukemia Baylar-HGSC project-TCBAP1D3842 Homo sapiens cDNA clone TCBAP3842
5189	10288	15433	0.87	2.0E-48	X67147.1	NT	Human endogenous retrovirus PHE.1 (ERV9)
55	5266	10394	11.85	1.0E-48	7708534	NT	Homo sapiens cisplatin resistance-associated overexpressed protein (LOC51747), mRNA
874	6025	11188	8.27	1.0E-48	4502188	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1077	6217	11381	2.48	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1077	6217	11382	2.48	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1300	6430	11604	4.11	1.0E-48	5032032	NT	Homo sapiens RNA binding motif protein 8 (RBM8) mRNA
1821	7040	12261	39.39	1.0E-48	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3469	8611	13777	0.91	1.0E-48	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
5113	10214	13351	1.22	1.0E-48	M10978.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
2007	7124	12360	1.23	8.0E-48	AB028497.1	NT	Mus musculus MyoPDZ mRNA for myosin containing PDZ domain, complete cds
135	5581	10704	2.55	7.0E-48	5728980	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, A (Pase, 4 (PSMC4) mRNA
135	5581	10705	2.55	7.0E-48	5728980	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
392	5561	10704	1.66	7.0E-49	5728990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
392	5561	10705	1.98	7.0E-49	5728990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
393	5561	10704	2.3	7.0E-49	5728990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
393	5561	10705	2.3	7.0E-49	5728990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
1223	6356	11625	4.13	7.0E-49	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
194	5389	10532	71.58	6.0E-49	AW731740.1	EST_HUMAN	ba55g05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800504 3' similar to gb:U17208 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20832 Mouse LLR3 protein mRNA from a repetitive element, complete (MOUSE);
1365	8494	11676	1.26	6.0E-49	BF038269.1	EST_HUMAN	601457738F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3861272 5'
1365	8494	11676	1.26	6.0E-49	BF038269.1	EST_HUMAN	601457738F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3861272 5'
710	5867	11013	7.34	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
710	5867	11014	7.34	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1806	6930	12145	2.24	5.0E-49	AA172121.1	EST_HUMAN	zp28c07.11 Stradgene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:610860 5' similar to TR:G233228 G233228 RTVL-H PROTEIN ; contains LTR7.9 LTR7 LTR7 repetitive element ;
2713	7608	13062	7.74	5.0E-49	U17714.1	NT	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds
3256	8408	13567	8.36	5.0E-49	11436355	NT	Homo sapiens similar to ribosomal protein S27 (metalloproteinase 1) (H. sapiens) (LOC63362), mRNA
523	5859	10820	23.9	4.0E-49	AW189633.1	EST_HUMAN	X08501.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2876593 3' similar to WP:B0350.2B
559	5724	10855	3.63	3.0E-49	X68598.1	NT	CE08703 ; H. sapiens mRNA for acetyl-CoA carboxylase
2609	7708		1.11	3.0E-49	AA016131.1	EST_HUMAN	z631c05.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1 repetitive element ;
4988	10076	16214	2.28	3.0E-49	U46939.1	NT	Human type IV collagen (COL4A8) gene, exon 40
660	5821		1.55	2.0E-49	BE165980.1	EST_HUMAN	MR3-HIT0487-150200-119-g01 HIT0487 Homo sapiens cDNA
3207	8358	13519	1.73	2.0E-49	N26448.1	EST_HUMAN	yc23408.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:282871 5'
3556	8697	13857	0.65	2.0E-49	AF026584.1	NT	Homo sapiens RNA binding protein II (RBMII) gene, complete cds
800	6050		9.82	1.0E-49	BF033327.1	EST_HUMAN	601458631F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862088 5'
1568	6696	11863	30.86	1.0E-49	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1813	6938	12162	3.89	1.0E-49	BE265216.1	EST_HUMAN	60111768F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356273 5'
4980	10038		1.67	9.0E-50	AF101475.1	NT	Homo sapiens glycine N-methyltransferase (GNMT) gene, complete cds
166	5391	10501	3.43	8.0E-50	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
717	5874	11021	1.6	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
717	5874	11022	1.6	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1034	6176		1.65	8.0E-50	AF000573.1	NT	Homo sapiens homogenized 1,2-dioxygenase gene, complete cds
1774	6900	12108	3.81	8.0E-50	4501890	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
2466	7669	12810	1.91	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51674), mRNA
2465	7559	12811	1.81	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51674), mRNA
2660	7759	13007	3.04	8.0E-50	4826659	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA
618	5776	10907	2.59	7.0E-50	BE089591.1	EST_HUMAN	QV0-BT0703-280400-211-c08 BT0703 Homo sapiens cDNA
8191	10288	16424	0.62	7.0E-50	BE087807.1	EST_HUMAN	QV1-BT0881-280400-181-g02 BT0881 Homo sapiens cDNA
8191	10288	15425	0.82	7.0E-50	BE087807.1	EST_HUMAN	QV1-BT0881-280400-181-g02 BT0881 Homo sapiens cDNA
4320	9442		0.73	6.0E-50	BE794381.1	EST_HUMAN	601589655F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5'
1805	6829	12143	1.36	5.0E-50	BF332838.1	EST_HUMAN	CM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
1805	6829	12144	1.36	5.0E-50	BF332838.1	EST_HUMAN	CM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
917	6068		2.42	4.0E-50	AA601143.1	EST_HUMAN	nc84608.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:U53741_mel
3430	8572	13732	0.96	4.0E-50	AL163248.2	NT	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1842	7061		2.01	3.0E-50	M19048.1	NT	Homo sapiens chromosome 21 segment HS21C048
2489	7593	12841	1.4	3.0E-50	BE259198.1	EST_HUMAN	601109717F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350309 5'
3281	8430	13692	0.63	3.0E-50	AA746142.1	EST_HUMAN	gb03106.s1 NCL_CGAP_K93 Homo sapiens cDNA clone IMAGE:1322627 3'
778	5932		5.43	2.0E-50	AF055088.1	NT	Homo sapiens MHC class 1 region
1081	6220	11388	6.34	2.0E-50	4567762	NT	Homo sapiens midline 1 (Optiz/BBB syndrome) (MID1) mRNA
1454	6981	11770	1.39	2.0E-50	AF138803.1	NT	Homo sapiens decorin D mRNA, complete cds, alternatively spliced
3271	8420	13581	1.06	2.0E-50	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds, and unknown genes
4234	9359	14491	0.68	2.0E-50	D88424.1	NT	Mus musculus mRNA for high-sulfur keratin protein, partial cds
4949	9981	16106	1.16	2.0E-50	AW869159.1	EST_HUMAN	MR3-SN0068-040500-008-f01 SN0068 Homo sapiens cDNA
4949	9981	16106	1.16	2.0E-50	AW869159.1	EST_HUMAN	MR3-SN0068-040500-008-f01 SN0068 Homo sapiens cDNA
481	5629	10768	1.82	1.0E-50	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2345	7452		4.95	1.0E-50	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
4540	9659	14802	6.31	8.0E-61	AA810842.1	EST_HUMAN	np88008.s1 NCL_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb:X12871_mel
2988	8143	13308	0.7	7.0E-61	AW274720.1	EST_HUMAN	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
3266	8415	13577	1.42	7.0E-61	AW869216.1	EST_HUMAN	Q92340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ;
3344	8480	13656	0.7	7.0E-61	AW274720.1	EST_HUMAN	Q92340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ;
4138	8263	14405	1.01	7.0E-61	AL078628.1	EST_HUMAN	Q92340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ;

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4138	6268	14408	1.01	7.0E-51	AL076828.1	EST_HUMAN	DKFZp434B2228_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B2228 6'
4328	9450	14583	1.33	7.0E-51	AW265803.1	EST_HUMAN	U1-H-BW0-clip-b-05-0-U1.st NCL_CGAP_Sub08 Homo sapiens cDNA clone IMAGE:2728817 3'
1542	6970	11858	1.02	8.0E-51	6878783	NT	Homo sapiens putative DNA binding protein (M88), mRNA
1991	7098	12329	3.03	8.0E-51	7857286	NT	Homo sapiens KIAA0828 protein Mx2 Interacting nuclear target (MINT) homolog (KIAA0828), mRNA
3455	8597	13761	13.36	8.0E-51	7857286	NT	Homo sapiens KIAA0929 protein Mx2 Interacting nuclear target (MINT) homolog (KIAA0929), mRNA
792	6948	11108	6.93	5.0E-51	AL183203.2	NT	Homo sapiens chromosome 21 segment HS21C003
804	5957	11120	1.73	5.0E-51	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
892	7908	11307	1.08	5.0E-51	AL13204.1	NT	Novel human gene mapping to chromosome X
1821	6749	11943	2.16	5.0E-51	5031880	NT	Homo sapiens 28S proteasome-associated pad1 homolog (POH1) mRNA
2555	7658	12909	6	5.0E-51	AJ075538.1	NT	Homo sapiens mRNA for nucleoporin 155
3916	9052	14211	1.63	6.0E-51	M80938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
3916	9052	14212	1.63	5.0E-51	M80938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5054	10156	15287	1.44	5.0E-51	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
130	5328	10474	57.38	3.0E-51	AI597348.1	EST_HUMAN	tr81609.x1 NCL_CGAP_Par1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M28328
1178	6313	11491	185.78	3.0E-51	AI597348.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
4303	9425	14560	1.89	3.0E-51	AL169142.1	NT	Novel human gene mapping to chromosome 22
384	5544	10886	5.18	2.0E-51	4507788	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
688	5844	10983	2.36	2.0E-51	BE391063.1	EST_HUMAN	601285594F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
688	5844	10984	2.36	2.0E-51	BE391063.1	EST_HUMAN	601285594F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
1702	8830	12032	4.18	2.0E-51	AA233392.1	EST_HUMAN	z30a05.1 StrataGene NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:664880 5' similar to TR:0233228 G233228 RTVL-H PROTEIN ; contains LTR7.3 LTR7 repetitive element ;
3714	8852	14006	2.49	2.0E-51	A482415.1	EST_HUMAN	627g03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131732 3'
4469	9588	14727	0.97	2.0E-51	AW137828.1	EST_HUMAN	U1-H-B1-adj-d-02-0-U1.st NCL_CGAP_Sub03 Homo sapiens cDNA clone IMAGE:2716891 3'
110	5314	10453	27.83	1.0E-51	4503528	NT	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
1506	6533		49.98	1.0E-51	AV742248.1	EST_HUMAN	AV742248 CB Homo sapiens cDNA clone CBFBCT12 5'
3168	8319	13461	1.41	1.0E-51	AF000994.1	NT	Homo sapiens ubiquitin TPR motif Y isoform (UTY) mRNA, alternative transcript 3, complete cds
147	5344	10487	8.69	8.0E-52	AA720574.1	EST_HUMAN	THR repetitive element ;
1510	6637	11824	1.7	8.0E-52	X84900.1	NT	H. sapiens mRNA for lamhin-6, alpha3b chain

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1667	6765	11690	1.87	8.0E-52	11688028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1667	6765	11691	1.87	8.0E-52	11688028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
3669	6765	11690	8.18	8.0E-52	11688028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
3669	6765	11691	8.18	8.0E-52	11688028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1189	6323		1.38	8.0E-52	BE072409.1	EST_HUMAN	QV3-BT0537-271289-049-007 BT0537 Homo sapiens cDNA
1707	6835	12036	2.13	8.0E-52	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4418	6538	14679	1.7	5.0E-52	Z78888.1	NT	H. sapiens flow-sorted chromosome 8 HindIII fragment, SCAP18H7
1675	6804	11009	1.24	4.0E-52	AF257318.1	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
1798	6523	12133	1.17	4.0E-52	4768843	NT	Homo sapiens nucleoprotein 165kD (NUP165) mRNA
3901	9037	14198	0.77	4.0E-52	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4068	9188		10.26	3.0E-52	11437042	NT	Homo sapiens hypothetical protein FLJ10675 (FLJ10675), mRNA
561	5728	10856	3.35	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
561	5728	10857	3.35	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1768	6894	12101	1.78	2.0E-52	AB000789.1	NT	Homo sapiens KIAA0439 mRNA, partial cds
2470	7574	12827	4.78	2.0E-52	BE207575.1	EST_HUMAN	b66807.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gbx1/0493 M.musculus mRNA for Zfp-1 zinc finger protein (MOUSE);
2698	7794		13.82	2.0E-52	BF677892.1	EST_HUMAN	602084710F1 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:4248891 5'
4982	10070	15208	4.18	2.0E-52	AL137188.3	NT	Novel human gene mapping to chromosome 20, similar to membrane transporters
5000	10105	15235	1.13	2.0E-52	A1141802.1	EST_HUMAN	qa6605.61 Soares_NIHMPU_S1 Homo sapiens cDNA clone IMAGE:1680784 3'
5090	10105	15236	1.13	2.0E-52	A1141802.1	EST_HUMAN	qa6605.61 Soares_NIHMPU_S1 Homo sapiens cDNA clone IMAGE:1680784 3'
551	5697	10830	1.3	1.0E-52	AA634445.1	EST_HUMAN	zu75h12.61 Soares_Isatis_NHT Homo sapiens cDNA clone IMAGE:743679 3'
1360	6508	11689	12.26	1.0E-52	4504028	NT	Homo sapiens glutamate-aminoligase (glutamine synthase) (GLUL) mRNA
2608	7611		1.78	1.0E-52	4502238	NT	Homo sapiens erythritolase D (ARSD), transcript variant 1, mRNA
3051	8185	19340	1.58	1.0E-52	S81070.1	NT	pcd-reverse transcriptase homolog (retroviral element) [human, endogenous retroviral element RTVL-Hip1, Genomic, 680 nt]
4370	8491	14635	0.63	8.0E-53	AF001446.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 3
5178	10278	15413	1.59	9.0E-53	AB040937.1	NT	Homo sapiens mRNA for KIAA1604 protein, partial cds
4074	9204	14340	7.43	5.0E-53	4758543	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA
48	5260	10384	1.49	4.0E-53	AL183286.2	NT	Homo sapiens chromosome 21 segment HS21C085

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Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
48	5260	10385	1.49	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4789	8902	15043	1.29	4.0E-53	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA
2821	7720	12974	1.42	3.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3712	8850	14004	0.89	3.0E-53	AW050808.1	EST_HUMAN	w22a07.x1 Scores_Dickgrafe_cdon, NHCD Homo sapiens cDNA clone IMAGE:2658788 3'
4563	8681	14820	1.22	3.0E-53	AW803583.1	EST_HUMAN	IL2-JM0081-240300-055-D03 UM0081 Homo sapiens cDNA
457	5825		3.25	2.0E-53	AA366598.1	EST_HUMAN	EST77528 Pancreas tumor III Homo sapiens cDNA 5' end
2308	7417	12687	16.62	2.0E-53	U76027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2509	7612		4.98	2.0E-53	4502316	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP8E), mRNA
2688	7785	13033	1.12	2.0E-53	4757815	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
2888	7785	13034	1.12	2.0E-53	4757815	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
4033	9164	14308	3.37	2.0E-53	M81873.1	NT	Human Krueppel-related DNA-binding protein (TF34) gene, partial cds
5193	10290	15427	1.4	2.0E-53	7662083	NT	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
1458	6585	11773	2.62	1.0E-53	AJ271738.1	NT	Homo sapiens Xq pseudosubosomal region; segment 22
3391	8535	13598	1.24	1.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4946	10054	15192	1.07	1.0E-53	BE293386.1	EST_HUMAN	601178725F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3831619 5'
204	5399	10541	4.55	8.0E-54	BE989785.1	EST_HUMAN	601272863F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3814031 5'
1849	6970	12191	1.84	8.0E-54	4504610	NT	Homo sapiens Insulin-like growth factor 2 receptor (IGF2R) mRNA
382	5591	10736	1.12	7.0E-54	AA812537.1	EST_HUMAN	af79c12.e1 Scores_testis_NHT Homo sapiens cDNA clone 1377048 3' similar to contains MER30.13 MER30 repetitive element;
1844	6955	12188	1.14	7.0E-54	Y16845.1	NT	Homo sapiens mRNA for monocyte chemotactic protein-2
2188	7300	12549	2.61	7.0E-54	N21777.1	EST_HUMAN	yw68d12.e1 Scores_placenta_8tdoWeeks_2NBA-IP8ts9W Homo sapiens cDNA clone IMAGE:257398 3' similar to contains LTR7.k3 LTR7 repetitive element;
23	5234	10348	1.12	6.0E-54	AB003618.1	NT	Homo sapiens DNA for MICB, exon 4, 5 and partial cds
383	5592	10737	1.03	8.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M033 (DKFZp434M033), mRNA
383	5592	10738	1.03	8.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3287	8416	13578	0.9	8.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3979	9113	14281	1.15	8.0E-54	4502872	NT	Homo sapiens chloride channel 8 (CLCN8) mRNA
4441	9560	14702	1.05	8.0E-54	AV754748.1	EST_HUMAN	AV754748 TP Homo sapiens cDNA clone TPGAAC10 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4812	8924	15065	2.14	8.0E-54	4505808	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4845	8937		1.47	6.0E-54	Y08846.1	NT	H. sapiens shc pseudogene, p68 isoform
4888	8957		2.77	6.0E-54	Y08846.1	NT	H. sapiens shc pseudogene, p68 isoform
2135	7249	12495	7.98	5.0E-54	P51623	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
178	5372		261.14	4.0E-54	AF110103.1	NT	Tupala belangeri beta-actin mRNA, partial cds
957	5105	11274	223.4	4.0E-54	AA308784.1	EST_HUMAN	EST117688 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
1817	6940	12167	2.26	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1817	6940	12168	2.26	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3187	8338		1.52	4.0E-54	AB35088.1	EST_HUMAN	w026411.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328269 3' similar to TRC002711
89	5288	10437	11.81	3.0E-54	AA313487.1	EST_HUMAN	O02711 PRO-POL-DUTPASE POLYPROTEIN:
2589	7690		1.02	3.0E-54	AB08757.1	EST_HUMAN	EST185371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
841	5802	10835	4.73	2.0E-54	5031800	NT	L-BY189-10339-007 BT180 Homo sapiens cDNA
1374	6502	11694	1.16	2.0E-54	4307164	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
1582	6691	11877	1.14	2.0E-54	AA655008.1	EST_HUMAN	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
2611	7614	12894	2.48	2.0E-54	AW183175.1	EST_HUMAN	n078a09.s1_NCI_CGAP_P3 Homo sapiens cDNA clone IMAGE:1204800 similar to contains element L1 repetitive element 1;
2584	7895	12820	1.03	2.0E-54	AL183210.2	NT	aug2g03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783784 5' similar to SW-CUL1_HUMAN Q13816 CULLIN HOMOLOG 1;
2861	8016	13182	1.16	2.0E-54	AW057524.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
3536	8877		8.84	2.0E-54	AA532825.1	EST_HUMAN	w060b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2652827 3' similar to TRC02084 Q62084 PHOSPHOLIPASE C NEIGHBORING;
3827	8963	14113	0.72	2.0E-54	4506376	NT	n045g09.s1_NCI_CGAP_P3 Homo sapiens cDNA clone IMAGE:905488 similar to gb-X63777 60S
3927	8993	14114	0.72	2.0E-54	4506376	NT	RIBOSOMAL PROTEIN L23 (HUMAN);
4177	9303		3.16	2.0E-54	4502842	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4419	9539		0.95	2.0E-54	AF208161.1	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4850	9982	15107	1.18	2.0E-54	7706446	NT	Homo sapiens chaperonin containing 1-complex subunit 6 (CCT6) mRNA
4444	9563		1.41	1.0E-54	BF316418.1	EST_HUMAN	Homo sapiens synovial precursor, mRNA, complete cds
1320	6449		0.72	8.0E-55	Y07828.2	NT	Homo sapiens peptidylarginine deaminase type III (LOC51702), mRNA
1323	6432		2.12	8.0E-55	Y07828.2	NT	601889230F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128635 6'
1780	6806	12113	1.39	6.0E-55	AA704971.1	EST_HUMAN	Homo sapiens RFB30 gene for RING finger protein
1780	6806	12114	1.39	6.0E-55	AA704971.1	EST_HUMAN	Homo sapiens RFB30 gene for RING finger protein
1780	6806	12114	1.39	6.0E-55	AA704971.1	EST_HUMAN	495509.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462817 3'
1780	6806	12114	1.39	6.0E-55	AA704971.1	EST_HUMAN	495509.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462817 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4737	9850	14997	1.57	5.0E-55	AW208021.1	EST_HUMAN	U1H-B11-674-g-09-0-U1H1 NCI_QGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723538 3'
54	7882	10393	3.01	4.0E-55	AW857894.1	EST_HUMAN	EST370064 MAGE resequences, MAGE Homo sapiens cDNA
671	6830	10970	31.27	4.0E-55	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM71A1) mRNA
1451	6579	11768	1.84	4.0E-55	7881713	NT	Homo sapiens predicted osteoblast protein (GS3788), mRNA
1451	6578	11767	1.54	4.0E-55	7881713	NT	Homo sapiens predicted osteoblast protein (GS3788), mRNA
1529	6656						752b10.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3390043 3' similar to contains L1.13 L1 repetitive element
2018	7135	12373	4.48	4.0E-55	BF081411.1	EST_HUMAN	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2018	7135	12374	4.48	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2078	7184	12437	3.73	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (DGKG) mRNA
2078	7184	12438	3.73	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (DGKG) mRNA
2287	7398	12848	7.71	4.0E-55	4507784	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA
3283	8412	13574	1.07	4.0E-55	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
376	6553	10697	2.83	2.0E-55	X57147.1	NT	Human endogenous retrovirus phiE.1 (ERV9)
550	5715		1.74	2.0E-55	MT0976.1	NT	Human endogenous retrovirus phiE.1 (ERV9)
648	5809	10844	3.88	2.0E-55	4507288	NT	Homo sapiens synaptobin-binding protein 1 (STXBP1) mRNA, and translated products
2826	8080	13248	2.08	2.0E-55	4507788	NT	Homo sapiens synaptobin-binding protein 1 (STXBP1) mRNA, and translated products
4741	9854	15001	2.82	2.0E-55	BE719988.1	EST_HUMAN	syndrome (UBE3A) mRNA
92	6301	10440	1.55	1.0E-55	4505080	NT	CM1-HT0878-150800-357-g03 HT0878 Homo sapiens cDNA
							Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA
188	5381	10522	78.12	1.0E-55	U08823.1	NT	Oryzopsis cuniculoides New Zealand white elongation factor 1 alpha (Rabef1a2) mRNA, complete cds
1151	6287	11452	3.98	1.0E-55	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1856	7072	12286	47.44	1.0E-55	BE277881.1	EST_HUMAN	601120118F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2887027 5'
1855	7072	12287	47.44	1.0E-55	BE277881.1	EST_HUMAN	601120118F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2887027 5'
2305	7414		4.47	1.0E-55	5803174	NT	Homo sapiens SMA3 (SMA3), mRNA
2488	7592	12840	9.54	1.0E-55	X13111.1	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2824	7627	12873	2.04	1.0E-55	AB007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2824	7627	12874	2.04	1.0E-55	AB007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2875	7675	12929	3.13	1.0E-55	L54057.1	NT	Homo sapiens CLP mRNA, partial cds
3390	8534	13895	0.97	1.0E-55	W28180.1	EST_HUMAN	43c-5 Human riba cDNA randomly primed sublibrary Homo sapiens cDNA
3964	9099	14246	3.8	1.0E-55	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C087
4270	8384	14633	1.18	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4698	9815		1.15	1.0E-55	N77281.1	EST_HUMAN	yv44g03.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245620 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4786	8809	15049	4.45	1.0E-55	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
4786	8809	15050	4.45	1.0E-55	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
5112	10213	16360	1.07	1.0E-55	8923126	NT	Homo sapiens hypothetical protein FLJ20126 (FLJ20126), mRNA
2695	7792	13042	3.22	7.0E-56	H18934.1	EST_HUMAN	Yn82g03.1 Soares adult brain N265HB55Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains THR repetitive element1
1708	6834	12035	1.43	5.0E-56	AW097712.1	EST_HUMAN	RC3-BN0053-170200-011-101 BN0053 Homo sapiens cDNA
26	5237	10351	28.3	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
26	5237	10362	28.3	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2155	7288		1.1	4.0E-56	BF207596.1	EST_HUMAN	601862059F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:4081551 5'
2670	7768	13017	6.1	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2670	7768	13018	6.1	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2773	5690	10822	5.49	4.0E-56	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2783	7879	12833	1.15	4.0E-56	AI632488.1	EST_HUMAN	w00908.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2305191 3' similar to SW-DCOR_MUSPA P27119 ORNITHINE DECARBOXYLASE
2788	7879	12834	1.15	4.0E-56	AI632488.1	EST_HUMAN	w00908.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2305191 3' similar to SW-DCOR_MUSPA P27119 ORNITHINE DECARBOXYLASE
1347	6478	11658	4.09	3.0E-56	8924029	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA
1776	6901	12109	4.35	3.0E-56	8912743	NT	Homo sapiens 5'3' exonuclease 2 (XRN2), mRNA
2134	7248	12494	1.14	3.0E-56	6912687	NT	Homo sapiens oncogene TC21 (TC21), mRNA
3102	8255	13405	1.85	3.0E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3102	8255	13406	1.85	3.0E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3812	8949		2.77	3.0E-56	AF050568.1	NT	Homo sapiens MHC class 1 region
3892	9028	14187	0.76	3.0E-56	BE383512.1	EST_HUMAN	601310203F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3681848 5'
4402	9522	14863	4	3.0E-56	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4545	9683	14808	2.31	3.0E-56	5902085	NT	Homo sapiens superkiller viralidid activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
622	5688		2.42	2.0E-56	AA180918.1	EST_HUMAN	zq52a08.e1 Striatogene neuroepithelium (#687231) Homo sapiens cDNA
731	7899	11037	2.24	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-016-F10 BT0310 Homo sapiens cDNA
731	7899	11038	2.24	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-016-F10 BT0310 Homo sapiens cDNA
2957	8111	13274	1.4	2.0E-56	AB037836.1	NT	Homo sapiens mRNA for KIAA1474 protein, partial cds
3287	8444		1.66	2.0E-56	AB006081.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3521	8662	13828	1.11	2.0E-56	AV703184.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ADBCFG10 5'
981	8127		3.5	1.0E-56	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1638	6863	11848	5.72	1.0E-56	AA263038.1	EST_HUMAN	z54b08.r1 Soares ovary tumor NIHOT Homo sapiens cDNA clone IMAGE:728137 5' similar to gb:A94854 INTERLEUKIN ENHANCER-BINDING FACTOR (HUMAN);
3652	6781	13949	1.81	1.0E-68	AW588833.1	EST_HUMAN	hg23c11.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2848462 3'
3652	6781	13948	1.81	1.0E-68	AW588833.1	EST_HUMAN	hg23c11.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2848462 3'
5015	10118	15251	1.04	1.0E-56	AI803162.1	EST_HUMAN	QV-BT077-130169-078 BT077 Homo sapiens cDNA
624	5784		1.74	9.0E-57	AW880885.1	EST_HUMAN	QVQ-010033-070300-152-N03 OT0033 Homo sapiens cDNA
295	5483	10625	2.62	8.0E-57	AW816405.1	EST_HUMAN	QV4-ST0234-181189-037-406 ST0234 Homo sapiens cDNA
685	6035	11208	7.79	8.0E-57	AW284599.1	EST_HUMAN	xt06d10.x1 NCI_CGAP_Bnf63 Homo sapiens cDNA clone IMAGE:2768261 3' similar to gb:U06875 INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
1828	6951	12173	1.46	8.0E-57	AA498109.1	EST_HUMAN	z61b12.r1 Soares_batis_NHT Homo sapiens cDNA clone IMAGE:767161 5'
2598	7698	12852	6.47	7.0E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
2598	7698	12853	6.47	7.0E-57	7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
3233	8383	13543	1.26	7.0E-57	7242168	NT	Homo sapiens NME7 (NME7), mRNA
3233	8383	13544	1.28	7.0E-57	7242168	NT	Homo sapiens NME7 (NME7), mRNA
3254	8404	13566	0.78	7.0E-57	6005979	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3855	8891	14147	1.61	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p41K230) mRNA, complete cds
3855	8891	14148	1.61	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p41K230) mRNA, complete cds
3734	8872	14024	2.03	4.0E-57	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4980	10096	15227	1.05	4.0E-57	BE783949.1	EST_HUMAN	601471228F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874136 5'
805	5858	11121	2.34	3.0E-57	4507788	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1396	6484		51.82	3.0E-57	AA230279.1	EST_HUMAN	nc13f07.x1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1008037 similar to SW_RS10_HUMAN
2389	7474	12728	1.39	3.0E-57	AA348335.1	EST_HUMAN	P48783 40S RIBOSOMAL PROTEIN S10.;
2684	7760	13011	1.49	3.0E-57	BE876822.1	EST_HUMAN	ES164770 Hippocampus II Homo sapiens cDNA 5' end
2684	7760	13012	1.49	3.0E-57	BE876822.1	EST_HUMAN	7638b10.x1 NCI_CGAP_CELL1 Homo sapiens cDNA clone IMAGE:3288443 3' similar to WP:Y47H8C.2 CE20263;
3674	8913		60.77	3.0E-57	AW853984.1	EST_HUMAN	7638b10.x1 NCI_CGAP_CELL1 Homo sapiens cDNA clone IMAGE:3288443 3' similar to WP:Y47H8C.2 CE20263;
4037	9168	14309	5.42	3.0E-57	P08547	SWISSPROT	RC3-CT0264-119300-027-410 CT0264 Homo sapiens cDNA
1443	5571	11768	1.17	2.0E-57	AI478904.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1515	5842	11828	1.6	2.0E-57	AF246219.1	NT	hm25c10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157618 3' similar to contains Alu repetitive element; Homo sapiens SNAPE protein kinase SNAK mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1515	6842	11828	1.8	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
2378	7484	12738	0.97	2.0E-57	BE172628.1	EST_HUMAN	MRO-HT05559-D10400-009-110 HT05559 Homo sapiens cDNA
2691	7788	13038	2.49	2.0E-57	AA848419.1	EST_HUMAN	ak02b02.s1 Soares_papillary thyroid carcinoma N10HPA Homo sapiens cDNA clone IMAGE:1404747 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
3420	8582		1.39	2.0E-57	AL163204.2	NT	Homo sapiens chromosome 21 segment HS27C004
3538	8880	13842	0.7	2.0E-57	R07702.1	EST_HUMAN	ye88h01.1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:125809 5'
3538	8880	13843	0.7	2.0E-57	R07702.1	EST_HUMAN	ye88h01.1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:125809 5'
3904	9040	14200	1.15	2.0E-57	BE073284.1	EST_HUMAN	MRO-BT0851-050300-103-b03 BT0851 Homo sapiens cDNA
4485	9604	14742	0.05	2.0E-57	AL163283.2	NT	Homo sapiens chromosome 21 segment HS27C083
2213	7325	12575	1.07	1.0E-57	AW503208.1	EST_HUMAN	UHF-BND-akt-g-07-QUL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
687	5749		15.12	8.0E-58	BE868715.1	EST_HUMAN	601445848F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3450211 5'
653	5814	10950	4.07	8.0E-58	AI798376.1	EST_HUMAN	134607.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN;
653	5814	10951	4.07	8.0E-58	AI798376.1	EST_HUMAN	134607.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN;
1868	6988	12211	1.51	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
1868	6988	12212	1.51	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
2844	8088		2.82	8.0E-58	7706132	NT	Homo sapiens DHHC1 protein (LOC51304), mRNA
4900	10011	15186	1.53	7.0E-58	BE206803.1	EST_HUMAN	ba05g04.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823510 5' similar to TR:Q81489 Q81489 DHM1 PROTEIN;
2234	7346	12601	1.02	6.0E-58	BE385061.1	EST_HUMAN	601309435F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3431000 5'
2355	7482	12718	8	6.0E-58	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
2866	8020	13186	0.96	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
2866	8020	13187	0.96	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
288	5486	10827	3.03	5.0E-58	4507334	NT	Homo sapiens synaptobrevin 1 (SYN1), mRNA
708	5885	11012	5.2	5.0E-58	BE763984.1	EST_HUMAN	RC4-NT0057-160800-018-b05 NT0057 Homo sapiens cDNA
1197	6331	11499	3.29	5.0E-58	AW797948.1	EST_HUMAN	CH3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1197	6331	11500	3.29	5.0E-58	AW797948.1	EST_HUMAN	CH3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1198	6331	11499	2.28	5.0E-58	AW797948.1	EST_HUMAN	CH3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1198	6331	11500	2.28	5.0E-58	AW797948.1	EST_HUMAN	CH3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
3304	8451	13613	3.85	5.0E-58	AA888183.1	EST_HUMAN	at88e07.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1603808 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4232	8357	14489	0.67	5.0E-58	A1636745.1	EST_HUMAN	ts89607.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2238468 3' similar to SW:PRO2_ACACA P18984 PROFILIN II:
371	5551	10694	5.7	4.0E-58	4502302	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP6O) mRNA
787	5851	11111	1.23	4.0E-58	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
1480	6807	11793	0.99	4.0E-58	4603848	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2541	7644	12894	1.03	4.0E-58	AF265555.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
2596	7697	12960	2.03	4.0E-58	U36251.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 3
3308	8453	13615	1	4.0E-58	D16470.1	NT	Human mRNA, Xq terminal portion
3721	8859	14012	1.02	4.0E-58	5031690	NT	Homo sapiens EGF-like repeats and disocidin I-like domains 3 (EDIL3), mRNA
333	5516	11703	2.83	3.0E-58	R17879.1	EST_HUMAN	XJ10622.1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:31693 5'
1396	6524	11703	1.81	3.0E-58	4768931	NT	Homo sapiens peptide YY (PYY) mRNA
3168	8309	13468	3.32	3.0E-58	BF660848.1	EST_HUMAN	602185789F1 NIH_JMGC_45 Homo sapiens cDNA clone IMAGE:4300943 5'
3168	8309	13468	3.32	3.0E-58	BF660848.1	EST_HUMAN	602185789F1 NIH_JMGC_45 Homo sapiens cDNA clone IMAGE:4300943 5'
940	6088	11256	8.84	2.0E-58	AF068624.1	NT	Homo sapiens 5-aminodevinate synthase 2 (ALAS2) gene, complete cds
1294	6423		39.27	2.0E-58	BE208632.1	EST_HUMAN	ts89607.x1 NIH_JMGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:U88391 60S RIBOSOMAL PROTEIN L6 (HUMAN); gb:U88391 M.musculus mRNA for TAX responsive element binding protein (MOUSE);
720	5877	11024	0.65	1.0E-58	M65134.1	NT	Human complement component C5 mRNA, 3' end
1089	8209	11372	6.88	1.0E-58	6274549	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22kD, B22) (NDUFB9), mRNA
1332	6461	11840	3.63	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGE resequences, MAGD Homo sapiens cDNA
1332	8481	11641	3.63	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGE resequences, MAGD Homo sapiens cDNA
1877	6808	12003	1.26	1.0E-58	BE468132.1	EST_HUMAN	lv10108.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:3166335 3'
2763	7857	13113	2.83	1.0E-58	4759169	NT	Homo sapiens viral regulatory element binding transcription factor 2 (SREBF2) mRNA
2781	7126	12361	1.46	1.0E-58	5174444	NT	Homo sapiens G protein-coupled receptor 69A (GPR69A) mRNA
3700	8838	13992	0.77	1.0E-58	4607628	NT	Homo sapiens transition protein 1 (during histone to protamine replacement) (TPP1) mRNA
4856	10063	16202	4.67	1.0E-58	A1141063.1	EST_HUMAN	oa43h01.x1 Soares NIH/MPu_S1 Homo sapiens cDNA clone IMAGE:1678129 3'
2211	7323	12573	48.86	8.0E-59	4607378	NT	Homo sapiens TATA box binding protein (TBP) mRNA
173	7884		2.08	6.0E-60	BF036327.1	EST_HUMAN	60145831F1 NIH_JMGC_68 Homo sapiens cDNA clone IMAGE:3862088 5'
1765	6891	12097	0.96	5.0E-59	AW157261.1	EST_HUMAN	au631405.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to TR-016786 075786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.:

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1705	6391	12088	0.96	5.0E-59	AW157281.1	EST_HUMAN	au93h05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2763655 3' similar to
3104	8257	13408	6.48	5.0E-59	AB07484.1	EST_HUMAN	TR:075789 075789 QANGUOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.;
4828	9748	14891	7.69	5.0E-59	X83497.1	NT	W48c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358836 3'
794	5948	11109	2.42	4.0E-59	D80006.1	NT	H.sapiens DNA for ZNF80-linked ERV9 long terminal repeat
1241	6371	11545	5.89	4.0E-59	4505818	NT	Human mRNA for KIAA0184 gene, partial cds
1241	6371	11545	5.89	4.0E-59	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 6-kinase, type II, beta (PIP5K2B) mRNA, and translated products
5184	10262	16401	1.74	4.0E-59	AB03047.1	EST_HUMAN	Homo sapiens phosphatidylinositol-4-phosphate 6-kinase, type II, beta (PIP5K2B) mRNA, and translated products
9	5220		4.88	3.0E-59	AW665924.1	EST_HUMAN	w632e12.x1 NC1_CGAP_G08 Homo sapiens cDNA clone IMAGE:2488928 3'
224	5417	10554	3.68	3.0E-59	7682247	NT	EST377682 IMAGE resequences, MAGI Homo sapiens cDNA
1725	6852	12056	6.78	3.0E-59	4505860	NT	Homo sapiens KIAA0690 gene product (KIAA0690), mRNA
1725	6852	12057	6.78	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLATe) mRNA
2120	7235	12477	4.6	3.0E-59	AB028035.1	NT	Homo sapiens plasminogen activator, tissue (PLATe) mRNA
2120	7235	12478	4.6	3.0E-59	AB028035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2792	7950	13082	1.01	3.0E-59	AF23299.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
3108	8259	13412	3.82	3.0E-59	4502014	NT	Homo sapiens NF1-2 pseudogene, exon 17
3108	8259	13413	3.82	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3804	8941	14089	1.71	3.0E-59	4508044	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
4659	9776	14921	1.35	3.0E-59	AL163284.2	NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA
4809	8921	15063	1.62	3.0E-59	7427622	NT	Homo sapiens chromosome 21 segment HS21C084
158	5355		15.3	1.0E-59	BE28411.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2582	7883		1.63	1.0E-59	AA748468.1	EST_HUMAN	601176757F1 NIH_MGC.17 Homo sapiens cDNA clone IMAGE:3531827 6'
783	5918	11076	2.32	8.0E-60	AW977946.1	EST_HUMAN	ca65h11.a1 NC1_CGAP_G081 Homo sapiens cDNA clone IMAGE:1309029 3' similar to TR:Q13537
1483	6810	11768	3.19	8.0E-60	4759159	NT	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
2162	7285	12513	5.26	8.0E-60	6174658	NT	EST388949 IMAGE resequences, MAGO Homo sapiens cDNA
2162	7285	12514	5.26	8.0E-60	6174658	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA
753	5909	11068	4.23	7.0E-60	AF055058.1	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
754	5909	11068	4.23	7.0E-60	AF055058.1	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
816	5969	11130	1.08	7.0E-60	4504634	NT	Homo sapiens MHC class I region
2119	7234	12476	2.98	7.0E-60	AF077188.1	NT	Homo sapiens MHC class I region
2746	7840	13085	1.02	7.0E-60	AB011153.1	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
							Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
							Homo sapiens mRNA for KIAA0581 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4150	8278	14413	2.53	7.0E-60	4505488	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
4548	6998	14808	0.84	7.0E-60	AF264760.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2169	7272	12520	1.47	6.0E-60	BE964974.2	EST_HUMAN	601668761R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886069 3'
80	6288	10428	1.9	5.0E-60	AI807917.1	EST_HUMAN	wf52d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
80	6289	10429	1.9	5.0E-60	AI807917.1	EST_HUMAN	wf52d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
2216	7328	12580	1.14	4.0E-60	AW503208.1	EST_HUMAN	UIHF-BNO-akt-g-07-Q-JUL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2216	7328	12581	1.14	4.0E-60	AW503208.1	EST_HUMAN	UIHF-BNO-akt-g-07-Q-JUL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2842	8098	12214	1.68	4.0E-60	AA289037.1	EST_HUMAN	EST11498 Uterus Homo sapiens cDNA 5' end similar to retrovirus-related pol
1870	6990	12215	3.4	3.0E-60	BE562811.1	EST_HUMAN	601338448F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1870	6990	12215	3.4	3.0E-60	BE562811.1	EST_HUMAN	601338448F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1880	7000		22.16	3.0E-60	6031180	NT	Homo sapiens protein (PHB) mRNA
4436	9555	14897	1.9	3.0E-60	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
28	5240	10368	1.44	2.0E-60	AY008285.1	NT	Homo sapiens edute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
1439	6580	11743	6.02	2.0E-60	Z11694.1	NT	H. sapiens 41kDa protein kinase related to rat ERK2
1735	6862	12084	1.24	2.0E-60	M24803.1	NT	Human bcl protein mRNA, 5' end
1743	6870	12074	1.14	2.0E-60	AY008285.1	NT	Homo sapiens edute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
2671	7767	13018	1.01	2.0E-60	AW878005.1	EST_HUMAN	EST1390114 MAGE resequences, MAGE Homo sapiens cDNA
3586	8707	13888	0.88	2.0E-60	4797887	NT	Homo sapiens v-rat murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
3889	9025	14183	0.86	2.0E-60	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
520	6988	10818	2.73	1.0E-60	BE176883.1	EST_HUMAN	PM3-HT0605-2702300-001-e08 HT0605 Homo sapiens cDNA
3879	9015	14172	0.92	1.0E-60	AU143389.1	EST_HUMAN	AU143389 Y78AA1 Homo sapiens cDNA clone Y78AA1001854 5'
4936	10046	15186	1.21	1.0E-60	AL163286.2	NT	Homo sapiens chromosome 21 segment HS21C088
1100	6238	11401	1.27	9.0E-61	AU118344.1	EST_HUMAN	AU118344 HEMBA1 Homo sapiens cDNA clone HEMBA1005683 5'
2631	7728	12985	1.01	8.0E-61	AW005478.1	EST_HUMAN	wf05b10.x1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:2606866 3'
2631	7728	12986	1.01	8.0E-61	AW005478.1	EST_HUMAN	wf05b10.x1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:2606866 3'
2817	8071		2.67	8.0E-61	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
123	5322	10468	0.66	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
123	5322	10467	0.66	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
263	5453	10591	2.73	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3835480 5'
812	5965	11127	1.88	6.0E-61	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3835480 5'
1326	8455	11633	11.99	6.0E-61	AF119860.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1640	8768	11682	1.17	6.0E-61	BE267400.1	EST_HUMAN	601109238F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3380145 5'

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ. ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1660	6788	11883	3.34	6.0E-61	AA59033.1	EST_HUMAN	in66h08.s1 NCI_CGAP_Lart Homo sapiens cDNA clone IMAGE:1088897 3'
3288	8437	13688	8.69	6.0E-61	AU130888.1	EST_HUMAN	AU130888 NT2RP3 Homo sapiens cDNA clone NT2RP3001283 5'
357	5538	10678	0.68	5.0E-61	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1692	6821	12020	3.02	5.0E-61	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3008	8162	13319	2.28	5.0E-61	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
3181	8932	13495	1.49	5.0E-61	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3884	9089		1.66	5.0E-61	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4988	5538	10679	0.65	5.0E-61	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4188	8912	14447	1.28	3.0E-61	BE390279.1	EST_HUMAN	601308785F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631220 5'
498	6885	10800	1.57	2.0E-61	8922828	NT	Homo sapiens hypodermal protein FLJ11028 (FLJ11028), mRNA
1215	6347	11517	3.89	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-401 HT0513 Homo sapiens cDNA
1216	6347	11618	3.89	2.0E-61	BE168410.1	EST_HUMAN	QV2-HT0513-060400-147-401 HT0513 Homo sapiens cDNA
1678	6808	12008	1.52	2.0E-61	NS3039.1	EST_HUMAN	y63d11.s1 8cates fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:248453 3' similar to
2804	7703		1.41	2.0E-61	N93937.1	EST_HUMAN	qb:128444 60S RIBOSOMAL PROTEIN L35A (HUMAN);
434	5603		0.68	1.0E-61	AL163203.2	NT	Y03F11.1 Scars melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270189 5'
773	8927	11088	1.22	1.0E-61	5453829	NT	Homo sapiens chromosome 21 segment HS21C003
1406	6533	11711	1.13	1.0E-61	AL163203.2	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L) mRNA
1869	6989	12213	3.34	1.0E-61	6005983	NT	Homo sapiens chromosome 21 segment HS21C003
2180	7263	12540	2.28	1.0E-61	AW827281.1	EST_HUMAN	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
2786	7953	13119	1.57	1.0E-61	BE396363.1	EST_HUMAN	MSR1 repetitive element;
3387	8502	13070	0.88	1.0E-61	7662318	NT	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
3713	8851	14005	1.52	1.0E-61	BE174455.1	EST_HUMAN	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
4417	9537	14677	0.88	1.0E-61	4769249	NT	QV2-HT0517-140300-077-g08 HT0517 Homo sapiens cDNA
4417	9537	14678	0.88	1.0E-61	4769249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4826	8938	15079	9.22	1.0E-61	AW288181.1	EST_HUMAN	UIH-BW0-q1b-08-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
4828	8938	15080	9.22	1.0E-61	AW288181.1	EST_HUMAN	UIH-BW0-q1b-08-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
4524	8842	14790	1.64	8.0E-62	AA630420.1	EST_HUMAN	cc66h11.s1 NCI_CGAP_QCB1 Homo sapiens cDNA clone IMAGE:1364725 3' similar to SW:POL_MLVRK
1108	6248	11409	1.12	7.0E-62	AV714334.1	EST_HUMAN	P31785 POL POLYPYPTOIN;
3490	8931	13788	0.7	7.0E-62	P17480	SWISSPROT	AV714334 DGB Homo sapiens cDNA clone DGBAMA08 5'
							NUCLEAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1)
							(AUTOANTIGEN NOR-80)

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2868	8122		1.44	8.0E-62	U08410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
3363	8510		4.59	6.0E-62	11418255	NT	Homo sapiens CGI-66 protein (CGI-66), mRNA
415	5583	10731	5.02	5.0E-62	AJ950528.1	EST_HUMAN	wx61e07.x1 NC1_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2647204 3' similar to SW:GG86_HUMAN
2383	7489	12742	2.82	5.0E-62	AJ271783.1	NT	Q08378 GOLGIN-85, contains element MER22 repetitive element;
2383	7489	12743	2.82	5.0E-62	AJ271783.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2562	7855	12906	1.11	6.0E-62	U39487.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2562	7855	12906	1.11	5.0E-62	U39487.1	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
3400	8544	13703	2.89	5.0E-62	4606788	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
4304	9426	14501	1.76	5.0E-62	AA431093.1	EST_HUMAN	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4332	8850		0.96	5.0E-62	AW905887.1	EST_HUMAN	zw78a09.e1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT
841	5883	11161	2.12	4.0E-62	AW161479.1	EST_HUMAN	P47245 NARDILYSIN
841	5883	11162	2.12	4.0E-62	AW161479.1	EST_HUMAN	RC5-NN1089-100500-021-H03 NN1089 Homo sapiens cDNA
842	5883	11161	2.44	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
842	5883	11162	2.44	4.0E-62	AW161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2435	7539	12782	4.32	4.0E-62	AJ827800.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
2435	7539	12783	4.32	4.0E-62	AJ827800.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
3380	8525		8.08	4.0E-62	4557887	NT	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
73	5282	10420	0.7	3.0E-62	AB040909.1	NT	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
3018	8172	13328	1.13	3.0E-62	AB040909.1	NT	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
3018	8172	13329	1.13	3.0E-62	AB040909.1	NT	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
3676	8814	13970	14.65	3.0E-62	X62888.1	NT	Human cyclophilin-related processed pseudogene
4948	10057	15185	228.4	3.0E-62	AF228180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1234	8385	11538	2.82	2.0E-62	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1048	8187	11864	1.22	1.0E-62	AF246640.1	NT	Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds
1559	6688	11875	10.74	1.0E-62	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1811	8934	12149	1.99	1.0E-62	AA025207.1	EST_HUMAN	af70e11.1 Scores_NHT-MIPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1 CE03453
2880	8034	13201	0.88	1.0E-62	AL039044.1	EST_HUMAN	DKFZp566F104_r1 568 (synonym: hncd2) Homo sapiens cDNA clone DKFZp566F104 5'
3405	8548		0.97	1.0E-62	AB040911.1	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
4501	8620	14762	1.87	1.0E-62	- 8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
336	5519	10855	2.1	9.0E-63	AW816405.1	EST_HUMAN	QV4-ST0234-181189-037-068 ST0234 Homo sapiens cDNA
4016	9148	14289	7.57	9.0E-63	AB002349.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4015	9148	14289	7.57	9.0E-63	AB002349.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
2384	7481	12717	18.68	8.0E-63	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3443	8585	13748	3.27	8.0E-63	AF188348.1	NT	Gallus gallus Dsch2 protein (Dsch2) mRNA, complete cds
3443	8585	13747	3.27	8.0E-63	AF188348.1	NT	Gallus gallus Dsch2 protein (Dsch2) mRNA, complete cds
4239	8344	14497	4.21	8.0E-63	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
930	6078		3.87	7.0E-63	AI872137.1	EST_HUMAN	wm55g11.x1 NC1_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439908 3'
3302	8449	13612	0.75	4.0E-63	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3786	8923	14072	1.16	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
3786	8923	14073	1.16	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
1939	7058	12280	2.85	3.0E-63	AB018290.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
2740	7834	13087	2.12	3.0E-63	J00310.1	NT	Human Mat-RNA-1 gene 1
2781	6373	11549	10.08	3.0E-63	8005983	NT	Homo sapiens zinc finger protein 144 (Maf-18) (ZNF144), mRNA
188	5383	10525	1.85	2.0E-63	U07804.1	NT	Human DNA topoisomerase I mRNA, partial cds
185	5390	10553	1.28	2.0E-63	4885228	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
497	5684		1.72	2.0E-63	4557624	NT	Homo sapiens glutamate-cysteine ligase (aspartate-glutamate synthetase), catalytic (72.8kD) (GLCLC) mRNA
827	6980	11148	2.85	2.0E-63	7857042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
1581	6710	11901	1.46	2.0E-63	AB030398.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1581	6710	11902	1.46	2.0E-63	AB030398.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1777	6983	12111	2.88	2.0E-63	BE110739.1	EST_HUMAN	801301827F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2638109 5'
3139	8286	13443	1.74	2.0E-63	- 4502186	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3259	8418	13580	2.28	2.0E-63	AF108718.1	NT	Homo sapiens chromosome 3 subtelomeric region
3882	9018	14175	3	2.0E-63	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
4835	9947	15091	1.36	2.0E-63	AF111187.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
1527	6854	11840	1.28	1.0E-63	F08485.1	EST_HUMAN	HSC2VD111 normalized infant brain cDNA Homo sapiens cDNA clone o-zvd11

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1627	6864	11841	1.29	1.0E-63	F08485.1	EST_HUMAN	HSC2VD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zrd11
4319	8441	14574	2.76	1.0E-63	F08485.1	EST_HUMAN	HSC2VD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zrd11
4319	8441	14575	2.76	1.0E-63	F08485.1	EST_HUMAN	HSC2VD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zrd11
1049	6189		13.88	8.0E-64	BE280768.1	EST_HUMAN	601155232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3136038 6'
3518	8657		0.86	7.0E-64	BE394321.1	EST_HUMAN	601311455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5'
4700	8816	14963	2.21	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
4700	8816	14964	2.21	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
1736	6863	12065	2.71	6.0E-64	AI651892.1	EST_HUMAN	wb51e07.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
1736	6863	12066	2.71	6.0E-64	AI651892.1	EST_HUMAN	wb51e07.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
3028	8262	13401	4.4	6.0E-64	AW028445.1	EST_HUMAN	wr13e03.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2629438 3'
3038	8262	13402	4.4	6.0E-64	AW028445.1	EST_HUMAN	wr13e03.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2629438 3'
821	5974	11137	3.78	6.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
821	5974	11138	3.78	6.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1343	6472	11652	1.14	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0803 protein, partial cds
1726	6853	12058	1.38	5.0E-64	U89395.1	NT	Human I(3)mb1 protein homolog mRNA, complete cds
2788	6817	11805	5.44	5.0E-64		NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2788	6817	11806	5.44	5.0E-64		NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
3930	9088	14222	7.57	5.0E-64	AF017435.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
4211	9336	14468	0.65	5.0E-64	AF016898.1	NT	Homo sapiens B-ATF gene, complete cds
4211	9336	14469	0.65	5.0E-64	AF016898.1	NT	Homo sapiens B-ATF gene, complete cds
5181	9336	14468	0.67	5.0E-64	AF016898.1	NT	Homo sapiens B-ATF gene, complete cds
5181	9336	14469	0.67	5.0E-64	AF016898.1	NT	Homo sapiens B-ATF gene, complete cds
2182	7265	12542	2.85	3.0E-64	C18893.1	EST_HUMAN	C18895 Human placenta cDNA (TFJwara) Homo sapiens cDNA clone GEN:569E02 6'
3237	8987	13549	0.71	3.0E-64	BE784381.1	EST_HUMAN	60168965F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 6'
3424	8568	13724	1.31	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 6'
3424	8568	13725	1.31	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 6'
1089	6228	11393	1.18	2.0E-64	AA603940.1	EST_HUMAN	af09d08.s1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1031151 3'
1404	6532	11770	1.92	2.0E-64	4757701	NT	Homo sapiens eIF4E-like cap-binding protein (eIFP) mRNA
2497	7601		1.3	2.0E-64	AI927030.1	EST_HUMAN	wb87b01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462281 3' similar to contains element L1 repetitive element;
2502	7605	12854	4.87	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
2502	7605	12855	4.87	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048

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Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3118	8270	13428	1.06	2.0E-64	4504068	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
3768	8903	14055	0.65	2.0E-64	AW958145.1	EST_HUMAN	EST370215 MAGE resequencing, MAGE Homo sapiens cDNA
3768	8903	14055	0.65	2.0E-64	AW958145.1	EST_HUMAN	EST370215 MAGE resequencing, MAGE Homo sapiens cDNA
255	5448	10584	1.7	1.0E-64	AF231819.1	NT	Homo sapiens chromosome 21 unknown mRNA
1789	8915	12122	68.19	1.0E-64	AI929419.1	EST_HUMAN	au00c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519138 3' similar to gb:U21688_cds1 PROTHYMOSIN ALPHA (HUMAN); contains element MSR1 repetitive element :
3498	8037	13804	4.48	1.0E-64	AF198779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 8, and synaptoophysin genes, complete cds; and L-type calcium channel α -
3572	8713	13873	1.18	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3572	8713	13874	1.18	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3877	8013	14170	0.88	1.0E-64	8922829	NT	Homo sapiens hypodermal protein FLJ11028 (FLJ11028), mRNA
1058	6189	11364	6.24	6.0E-65	AV721898.1	EST_HUMAN	AV721898 HTB Homo sapiens cDNA clone HTB8ZC08 5'
1927	7048		40.69	6.0E-65	AA650929.1	EST_HUMAN	rib8d10.s1 NCI CGAP P11 Homo sapiens cDNA clone IMAGE:988378 similar to gb:K03002 60S
630	5780	10523	1.77	5.0E-65	AF094604.1	NT	Homo sapiens KE03 protein mRNA, partial cds
1360	6489	11639	1.61	5.0E-65	7681951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
1360	6489	11670	1.61	5.0E-65	7681951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
2138	7252	12498	0.89	5.0E-65	AB033768.1	NT	Homo sapiens NPAD-cadherin10 mRNA for peptidylarginine deiminase type I, complete cds
3238	8388	13560	1.89	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3238	8388	13551	1.89	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
190	5385	10528	2.69	4.0E-65	AL120418.1	EST_HUMAN	DKFZp761G108_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108 5'
744	5900	11053	1.12	4.0E-65	AI288468.1	EST_HUMAN	qm48e01.x1 Soares_placenta_8105weeks_2NbpHP8b9W Homo sapiens cDNA clone IMAGE:1891800 3'
744	5900	11054	1.12	4.0E-65	AI288468.1	EST_HUMAN	qm48e01.x1 Soares_placenta_8105weeks_2NbpHP8b9W Homo sapiens cDNA clone IMAGE:1891800 3'
1080	8219	11395	1.97	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FMR1), mRNA
1498	6923	11811	21.94	4.0E-65	4506838	NT	Homo sapiens ribosomal protein L34 (RPL34) mRNA
2318	7426	12677	2.41	4.0E-65	BE221468.1	EST_HUMAN	hu25604.x1 NCI CGAP_Ma15 Homo sapiens cDNA clone IMAGE:3171102 3'
2318	7426	12678	2.41	4.0E-65	BE221468.1	EST_HUMAN	hu25604.x1 NCI CGAP_Ma15 Homo sapiens cDNA clone IMAGE:3171102 3'
3922	9058	14217	0.98	4.0E-65	AW993185.1	EST_HUMAN	RC2-BND033-160200-013-e03 BND033 Homo sapiens cDNA
5167	10265	15405	0.82	4.0E-65	9055289	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI), mRNA
5167	10265	15406	0.82	4.0E-65	9055289	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI), mRNA

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
93	5303	10443	1.88	3.0E-65	5031978	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
94	5303	10443	1.37	3.0E-65	5031978	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1235	7870		27.41	3.0E-65	X78832.1	NT	H. sapiens HZF9 mRNA for zinc finger protein
1573	8701	11889	3.1	3.0E-65	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1834	8857	12179	1.48	3.0E-65	A1000692.1	EST_HUMAN	ov23f03.e1 Scarses_testis_NHT Homo sapiens cDNA clone IMAGE:1838173 3' similar to contains element
2059	8113	13275	1.49	3.0E-65	D87078.2	NT	MSR1 repetitive element;
3280	8409	13572	0.8	3.0E-65	4504850	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
3701	8839	13693	1.47	3.0E-65	A1000692.1	EST_HUMAN	Homo sapiens laminin, beta 1 (LAMB1), mRNA
4518	9738	14874	1.39	3.0E-65	6912385	NT	ov23f03.e1 Scarses_testis_NHT Homo sapiens cDNA clone IMAGE:1838173 3' similar to contains element
3385	8529	13691	5.17	2.0E-65	BF880284.1	EST_HUMAN	MSR1 repetitive element;
88	5296		2.03	1.0E-65	BF125544.1	EST_HUMAN	Homo sapiens rab8 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA
637	5703	10836	2.68	1.0E-65	7657495	NT	602155082F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295968 6'
2034	7152	12392	1.95	1.0E-65	AB040548.1	NT	601763498F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4028501 6'
3354	8489	13687	1.15	1.0E-65	BE466381.1	EST_HUMAN	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
3973	9107	14255	2.13	1.0E-65	4504082	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
4179	8905	14440	2.1	1.0E-65	AW028340.1	EST_HUMAN	h224e09.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:3208888 3'
4178	8305	14441	2.1	1.0E-65	AW028340.1	EST_HUMAN	Homo sapiens glycylalanine 4 (GPC4) mRNA
70	5280	10416	1.38	9.0E-66	AL160311.1	NT	Homo sapiens glycylalanine 4 (GPC4) mRNA
1361	8490	11671	2.88	9.0E-66	5031980	NT	Novel human gene mapping to chromosome 22
1361	8490	11672	2.88	9.0E-66	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1494	8621		5.38	9.0E-66	M87289.1	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
4344	9469	14602	1.18	6.0E-66	A1924653.1	EST_HUMAN	Human transposon-like element, partial
4344	9469	14603	1.18	6.0E-66	A1924653.1	EST_HUMAN	wn57n07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP-F15G9.4A
4344	9469	14604	1.18	6.0E-66	A1924653.1	EST_HUMAN	CE18595;
1378	8504	11688	1.84	5.0E-66	BE064410.1	EST_HUMAN	wn57n07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP-F15G9.4A
5091	10191	15330	2.25	5.0E-66	BE69844.1	EST_HUMAN	wn57n07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP-F15G9.4A

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6091	10191	15331	2.25	5.0E-68	BE888844.1	EST_HUMAN	601881502F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951791 5'
791	5945	11105	0.87	4.0E-68	6878816	NT	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA
2267	7387	12823	1.81	4.0E-68	X88211.1	NT	H. sapiens DNA for endogenous retroviral like element
2448	7553		2.75	4.0E-68	AJ223394.1	NT	Homo sapiens germ-line DNA upstream of Jkappa locus
4761	8804		4.83	4.0E-68	6835487	NT	Human endogenous retrovirus, complete genome
1438	6563	11747	28.39	3.0E-68	4502068	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC28A5), nuclear gene encoding mitochondrial protein, mRNA
1438	6563	11748	28.39	3.0E-68	4502068	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (SLC28A5), nuclear gene encoding mitochondrial protein, mRNA
1884	7101	12332	1.1	3.0E-68	N65323.1	EST_HUMAN	Y277g12.1 Soares_multiple_sclerol_2/NbHMSF Homo sapiens cDNA clone IMAGE:284328 5' similar to SW-H2B1_TIGCA P35068 HISTONE H2B.1H2B.2. [2] PIR:B66912;
1884	7101	12333	1.1	3.0E-68	N55323.1	EST_HUMAN	Y277g12.1 Soares_multiple_sclerol_2/NbHMSF Homo sapiens cDNA clone IMAGE:284328 5' similar to SW-H2B1_TIGCA P35068 HISTONE H2B.1H2B.2. [2] PIR:B66912;
1884	7101	12334	1.1	3.0E-68	N55323.1	EST_HUMAN	Y277g12.1 Soares_multiple_sclerol_2/NbHMSF Homo sapiens cDNA clone IMAGE:284328 5' similar to SW-H2B1_TIGCA P35068 HISTONE H2B.1H2B.2. [2] PIR:B66912;
2889	7765	13018	4.38	3.0E-68	11141880	NT	Homo sapiens TGF-beta-induced transcription factor 2 (TGIF2), mRNA
3093	8248	13398	6.6	3.0E-68	7682223	NT	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
50	5262	10387	2	2.0E-68	7657334	NT	Homo sapiens Mischapen/NIK-related kinase (MINIK), mRNA
50	5262	10388	2	2.0E-68	7657334	NT	Homo sapiens Mischapen/NIK-related kinase (MINIK), mRNA
421	5208	10320	0.89	2.0E-68	4506524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
421	5208	10321	0.89	2.0E-68	4506524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
1839	6860	12183	2.4	2.0E-68	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
3508	8847	13813	1.16	2.0E-68	8923280	NT	Homo sapiens hypothalamic protein FLJ20308 (FLJ20308), mRNA
3745	8883	14033	1.02	2.0E-68	AL117283.1	NT	Novel human gene mapping to chromosome 1
4826	9743	14888	5.12	2.0E-68	AJ133287.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
4826	9743	14887	5.12	2.0E-68	AJ133287.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
1897	6825		1.77	1.0E-68	BE887173.1	EST_HUMAN	601508376F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908831 5'
2880	8015	13180	1.52	1.0E-68	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
2880	8015	13181	1.52	1.0E-68	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4384	8015	13180	2.97	1.0E-68	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'
4384	8015	13181	2.97	1.0E-68	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADC07 5'

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Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4891	10002		0.61	8.0E-67	M78198.1	EST_HUMAN	EST01760 Subtracted Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCN31 similar to L1 repetitive element
378	5587	10732	1.89	7.0E-67	AW162232.1	EST_HUMAN	eu75602.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1392	6320	11700	2.26	7.0E-67	AA383416.1	EST_HUMAN	EST08812 Testis 1 Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid ZK353
1569	6697	11884	4.25	7.0E-67	W85947.1	EST_HUMAN	zh56005.r1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1569	6697	11885	4.25	7.0E-67	W85947.1	EST_HUMAN	zh56005.r1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
2027	7144	12383	2.28	7.0E-67	7857243	NT	Homo sapiens Inositol 1,3,4-trisphosphate 5/8 kinase (ITPK1), mRNA
2027	7144	12384	2.28	7.0E-67	7857243	NT	Homo sapiens Inositol 1,3,4-trisphosphate 5/8 kinase (ITPK1), mRNA
2771	5587	10732	2.33	7.0E-67	AW162232.1	EST_HUMAN	eu75602.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
558	5723	10854	8.35	6.0E-67	X68938.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
768	5950	11110	1.68	6.0E-67	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
1277	6408	11680	0.98	6.0E-67	Y14320.1	NT	Homo sapiens PMP39 gene, exons 3, 4, 5 & 7
3147	8288	13458	1.28	6.0E-67	4506434	NT	Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1) mRNA
3418	8561	13718	1.21	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
3419	8561	13719	1.21	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
4097	9228	14391	0.88	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4097	9228	14392	0.88	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4673	9789	14834	2.84	6.0E-67	7857020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
4673	9789	14835	2.84	6.0E-67	7857020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
5157	10257	15395	0.99	6.0E-67	AF018998.1	NT	Homo sapiens B-ATF gene, complete cds
5157	10257	15398	0.99	6.0E-67	AF018998.1	NT	Homo sapiens B-ATF gene, complete cds
3206	8387	13618	2.83	6.0E-67	AF009680.1	NT	Homo sapiens T cell receptor beta locus, TCRBV733A2 to TCRBV1232 region
1333	6482	11842	3.95	4.0E-67	R80819.1	EST_HUMAN	yn02811.r1 Soares adult brain N2b-4H8557 Homo sapiens cDNA clone IMAGE:167263 5'
2774	5762	10928	1.33	3.0E-67	AA333788.1	EST_HUMAN	EST03811.1 Embryo, 8 week Homo sapiens cDNA 5' end
3435	8577	13737	1.12	3.0E-67	BE084410.1	EST_HUMAN	RC4-BT0311-141189-011-H06 BT0311 Homo sapiens cDNA
4683	9779	14923	2.28	3.0E-67	AW899169.1	EST_HUMAN	MR3-SN0066-040500-008-01 SN0066 Homo sapiens cDNA
4690	9806		0.92	3.0E-67	AL163276.2	NT	Homo sapiens chromosome 21 segment HS21C079
184	5379	10520	1.33	2.0E-67	BE348394.1	EST_HUMAN	hw1809.x1 NCI_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183138 3' similar to WP:F23H11.9 CE08817;
846	5987	11168	3.92	2.0E-67	AW816405.1	EST_HUMAN	QV4-S10234-181189-037-405 S10234 Homo sapiens cDNA
1108	6244		1.98	2.0E-67	AF167460.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4

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1892	7011	12232	1.51	2.0E-67	BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2805976 5' similar to TR:094892 O94892 KIAA0768 PROTEIN ;
1892	7011	12233	1.51	2.0E-67	BE303037.1	EST_HUMAN	ba72g05.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2805976 5' similar to TR:094892 O94892 KIAA0768 PROTEIN ;
2221	7333	12588	1.11	2.0E-67	11422848	NT	Homo sapiens hypothetical protein dJ462023.2 (DJ462023.2), mRNA
2221	7333	12587	1.11	2.0E-67	11422848	NT	Homo sapiens hypothetical protein dJ462023.2 (DJ462023.2), mRNA
2384	7470	12728	2.48	2.0E-67	AF036681.1	NT	Homo sapiens KRAB zinc finger protein ZFOR mRNA, complete cds
2409	7516	12765	2.21	2.0E-67	4758795	NT	Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1), mRNA
3449	8591	13765	3.92	2.0E-67	AA625755.1	EST_HUMAN	zu91g01.s1 Soares_bat1e_NHT Homo sapiens cDNA clone IMAGE:743392 3'
3977	9111	14259	2.44	2.0E-67	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21G100
250	5441	10581	4.73	1.0E-67	4502188	NT	Homo sapiens amyloid beta (A4) precursor protein (protease resistant) (APP), mRNA
706	5863	11010	1.9	1.0E-67	AA702784.1	EST_HUMAN	z880b04.s1 Soares_fetaj_liver spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
4879	9795	14040	0.6	1.0E-67	BF438247.1	EST_HUMAN	na65108.x1 Soares_NSF_P8_9W_OT_PA_S1 Homo sapiens cDNA clone IMAGE:3'
2156	7269	12517	4.77	8.0E-68	BE870732.1	EST_HUMAN	601448558F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3852284 5'
3848	8984	14139	5.22	8.0E-68	AA209458.1	EST_HUMAN	z882h10.1 Strabagene tNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07590 SAV PROTEIN ;
3848	8984	14140	5.22	8.0E-68	AA209458.1	EST_HUMAN	z882h10.1 Strabagene tNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07590 SAV PROTEIN ;
1899	7018	11135	1.22	8.0E-68	AW503842.1	EST_HUMAN	ULHF-BNO-elb-c-07-0-UL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078824 5'
805	7866	11118	0.72	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
803	7866	11119	0.72	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
820	5973	11135	3.62	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
820	5973	11136	3.62	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
2741	7836	13088	38.26	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3125	8277	13433	2.97	5.0E-68	AB037652.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
4152	9278	13433	0.76	5.0E-68	4826897	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
2496	7602	12849	1.27	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
2498	7602	12850	1.27	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
3084	8217		1.12	4.0E-68	AW207003.1	EST_HUMAN	UH-B11-afdc-c-08-Q-UI.s1 NC1 CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721399 3'
4960	10068		19.6	4.0E-68	P04406	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
3638	8777	13802	5.78	3.0E-68	AF236082.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
2825	10313		32.61	2.0E-68	D00522.1	NT	Citellus longicaudatus mRNA for EF-1 alpha, complete cds

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Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3988	9132	14276	0.7	2.0E-68	BE675768.1	EST_HUMAN	71602.X1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3294747 3' similar to TR:080828 080828
4653	9770	14916	2.05	2.0E-68	AB000891.1	NT	HYPOTHETICAL 68.8 KD PROTEIN ;
284	5482	10624	11.03	1.0E-68	AW616405.1	EST_HUMAN	Homo sapiens gene for activin receptor type IIB, complete cds
2232	7344	12698	1.34	1.0E-68	AB011149.1	NT	QV4-ST0234-161189-037-035 ST0234 Homo sapiens cDNA
2232	7344	12698	1.34	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2720	7815	13071	1.16	1.0E-68	AW461832.1	EST_HUMAN	Homo sapiens mRNA for KIAA0577 protein, complete cds
3886	9119	14268	1.54	1.0E-68	BE286032.1	EST_HUMAN	U1H-B18-alk-f-01-Q-U1.1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731727 3'
5055	10157	15288	1.39	1.0E-68	BE286032.1	EST_HUMAN	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5'
20	5231	10343	8.71	9.0E-69	5031976	NT	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5'
20	5231	10344	8.71	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1029	6170	11335	1.66	9.0E-69	5031980	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1029	6170	11338	1.68	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
4100	8229	14368	0.66	9.0E-69	4757897	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
3367	8512		1.14	8.0E-69	AJ237744.1	NT	Homo sapiens v-rat murine sarcoma viral oncogene homolog B1 (BRAP) mRNA
518	6894		0.98	4.0E-69	AJ873630.1	EST_HUMAN	Homo sapiens RUBIK gene (partial), exon 12
384	5593	10739	5.27	3.0E-69	BE258012.1	EST_HUMAN	hm28h11.X1 NCI_CGAP_UM Homo sapiens cDNA clone IMAGE:2437125 3'
609	5759	10898	1.98	3.0E-69	AF221712.1	NT	601110371F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351352 5'
							Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
1570	6598		1.54	3.0E-69	T80514.1	EST_HUMAN	y08a02.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24880 5' similar to SP-A48838
4940	10050	15188	0.97	3.0E-69	AB037732.1	NT	A48838 SPEGF III-EGF REPEAT-CONTAINING FIBROBLAST-LIKE PROTEIN - SEA URCHIN ;
5126	9189	14330	0.95	3.0E-69	AJ765888.1	EST_HUMAN	Homo sapiens mRNA for KIAA1311 protein, partial cds
124	5571	10718	2.22	2.0E-69	AF160252.1	NT	hm68g08.X1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385758 3'
124	5571	10719	2.22	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
404	5571	10719	4.66	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
404	5571	10719	4.66	2.0E-69	AF160252.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
1893	7012	12234	2.34	2.0E-69	BE257857.1	EST_HUMAN	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
2806	7062		3.98	2.0E-69	AA431157.1	EST_HUMAN	601109444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350074 5'
1718	6845	12048	1.61	1.0E-69	AF053763.1	NT	zr71g02.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:271682 5'
2313	7837	12872	2.34	8.0E-70	AA230303.1	EST_HUMAN	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
4352	9474	14612	1.7	8.0E-70	L77568.1	NT	hm13d12.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008023
1825	6948	12169	3.57	7.0E-70	AJ497807.1	EST_HUMAN	Homo sapiens DGS-1 mRNA, 3' end
1825	6948	12170	3.67	7.0E-70	AJ497807.1	EST_HUMAN	hm8901.X1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3'
							hm8901.X1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3'

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	QRF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1835	7054	12276	1.88	7.0E-70	AA282955.1	EST_HUMAN	z15h04.r1 NCL_CGAP_GGB1 Homo sapiens cDNA clone IMAGE:713239 5'
2056	7172		6.1	7.0E-70	5031968	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-IR) mRNA
4202	8327	14459	3.42	7.0E-70	4757723	NT	Homo sapiens edarvylate cyclase 3 (ADCY3) mRNA
872	6023	11104	3.49	6.0E-70	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (precursor neuro-I, Alzheimer disease) (APP), mRNA
2126	7239	12482	5.6	6.0E-70	M30638.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
2478	7684	12834	2.07	6.0E-70	8923699	NT	Homo sapiens CNP-N-acetylneuraminic acid synthase (LOC55607), mRNA
2523	7942	12871	3.38	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
2623	7942	12872	3.38	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
1802	6730	11921	5.33	3.0E-70	BE071798.1	EST_HUMAN	RCO-BT0522-071289-011-a12 BT0522 Homo sapiens cDNA
6137	10237	15373	0.94	3.0E-70	BE071798.1	EST_HUMAN	RCO-BT0522-071289-011-a12 BT0522 Homo sapiens cDNA
37	9248	10369	1.24	2.0E-70	AF012872.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
687	5945	10985	13.85	2.0E-70	N42161.1	EST_HUMAN	Y07a10.r1 Soares melanocyte 2NHHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P28268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
687	5945	10986	13.85	2.0E-70	N42161.1	EST_HUMAN	Y07a10.r1 Soares melanocyte 2NHHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HL_RAT P28268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
703	5960	11009	2.51	2.0E-70	A1248599.1	EST_HUMAN	gp51h01.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004913 3'
1022	6163	11329	1.78	2.0E-70	8923699	NT	Homo sapiens hypothetical protein FLJ20788 (FLJ20788), mRNA
1186	6320	11488	4.33	2.0E-70	7661983	NT	Homo sapiens KIAA0183 gene product (KIAA0183), mRNA
1186	6320	11489	4.33	2.0E-70	7661983	NT	Homo sapiens KIAA0183 gene product (KIAA0183), mRNA
1754	6980	12086	1.41	2.0E-70	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2298	7407		4.84	2.0E-70	AA054010.1	EST_HUMAN	z148g04.r1 Soares retina N2B4HR Homo sapiens cDNA clone IMAGE:380214 5' similar to SW:GAG_HTL1A
2460	7684	12817	1.35	2.0E-70	AB011173.1	NT	P03346 GAG POLYPROTEIN ;
3797	8934	14081	2	2.0E-70	AL133207.2	NT	Homo sapiens mRNA for KIAA0601 protein, partial cds
4023	9155	14289	4.56	2.0E-70	M69181.1	NT	Novel human gene mapping to chromosome X
4164	9280	14426	0.9	2.0E-70	L78810.1	NT	Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds
4164	9280	14427	0.9	2.0E-70	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
3374	8519		3.07	1.0E-70	4507476	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
2192	7304	12554	31.81	6.0E-71	AF056322.1	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
4092	8221	14368	1.07	6.0E-71	AW818405.1	EST_HUMAN	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
100	5309	10449	0.9	4.0E-71	4507592	NT	QV4-ST0234-181169-037-R05 ST0234 Homo sapiens cDNA
							Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
347	5530	10688	331.53	4.0E-71	AF157628.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
347	5530	10689	331.53	4.0E-71	AF157628.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2845	8000	13189	1.01	4.0E-71	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA
2845	8000	13190	1.01	4.0E-71	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA
2853	8008	13188	2.01	4.0E-71	4503880	NT	Homo sapiens plasminogen (PLG) mRNA
4406	9528	14686	5.16	4.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4971	10079	15216	5.78	4.0E-71	7657802	NT	Homo sapiens putative heme-binding protein (SOUL), mRNA
1233	6364	11637	6.91	2.0E-71	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008 oy15a03.s1 Soares, senescent, fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1665016 3' similar to contains LOR1.b2 LOR1 repetitive element;
637	5788	10932	1.78	1.0E-71	AJ077827.1	EST_HUMAN	Homo sapiens neuronal cell death-related protein (LOC51616), mRNA
941	6089	11257	3.28	1.0E-71	7706281	NT	Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds
1101	6239	11402	3.42	1.0E-71	AF205890.1	NT	Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds
1346	6474	11654	8.13	1.0E-71	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2076	7191	12434	3.22	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2076	7191	12435	3.22	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2684	7762	13001	2.34	1.0E-71	7657183	NT	Homo sapiens hairyenhancer-3' split related with YRPW motif-like (HEYL), mRNA
3484	8825	13782	2	1.0E-71	AF118695.1	NT	Homo sapiens inorganic pyrophosphatase mRNA, complete cds
3692	8723	13880	5.81	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3582	8723	13881	5.81	1.0E-71	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3826	8765	13920	0.83	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3826	8765	13921	0.83	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3722	8890	14013	2.47	1.0E-71	AF218904.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 19
4449	9568	14709	1.82	1.0E-71	D28476.1	NT	Human mRNA for KIAA0046 gene, complete cds
407	5574	10721	0.89	9.0E-72	AJ857635.1	EST_HUMAN	wk85g03.x1 NCL CGAP Lu18 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O88705 O88705 HYPOTHETICAL 38.6 KD PROTEIN; contains Alu repetitive element
407	5574	10722	0.89	9.0E-72	AJ857635.1	EST_HUMAN	wk85g03.x1 NCL CGAP Lu18 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O88705 O88705 HYPOTHETICAL 38.6 KD PROTEIN; contains Alu repetitive element
4088	9216	14350	1.61	7.0E-72	4501866	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4088	9216	14351	1.61	7.0E-72	4501866	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4088	8216	14352	1.61	7.0E-72	4501868	NT	Homo sapiens acylase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
62	5273	10407	2.15	5.0E-72	BF333707.1	EST_HUMAN	QV0-C50010-150800-388-e11 CS0010 Homo sapiens cDNA
62	5273	10408	2.15	5.0E-72	BF333707.1	EST_HUMAN	QV0-C50010-150800-388-e11 CS0010 Homo sapiens cDNA
63	5273	10407	8.82	5.0E-72	BF333707.1	EST_HUMAN	QV0-C50010-150800-388-e11 CS0010 Homo sapiens cDNA
63	5273	10408	8.82	5.0E-72	BF333707.1	EST_HUMAN	QV0-C50010-150800-388-e11 CS0010 Homo sapiens cDNA
1140	6277		1.83	5.0E-72	L11845.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
4760	6803		1.2	4.0E-72	11034844	NT	Homo sapiens hypothetical protein dJ1057B20.2 (D1057B20.2), mRNA
19	5230	10342	2.05	3.0E-72	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
604	6064		0.93	3.0E-72	AA73823.1	EST_HUMAN	ab63408.e1 Scores_basile_NHT Homo sapiens cDNA clone 1310280 3'
1156	6282	11455	7.41	3.0E-72	U16308.1	NT	Human chondroitin sulfate proteoglycan variant V0 splice-variant precursor peptide mRNA, complete cds
1156	6282	11456	7.41	3.0E-72	U16308.1	NT	Human chondroitin sulfate proteoglycan variant V0 splice-variant precursor peptide mRNA, complete cds
1196	6330	11497	1.48	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1196	6330	11498	1.48	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1534	6661	11847	1.1	3.0E-72	BE242161.1	EST_HUMAN	TCAAP1E1262 Podiatris acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1262
3048	8200	13366	10.6	3.0E-72	AJ28043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3262	8411	13573	2.73	3.0E-72	8823548	NT	Homo sapiens hypothetical protein FLJ20586 (FLJ20586), mRNA
3601	8938	14085	2.78	3.0E-72	S77689.1	NT	TOR V delta 2-C alpha -T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction)
4395	9515	14656	1.1	3.0E-72	AF143892.1	NT	Human, precursor B-cell line REH, mRNA Partial, 211 nt
4396	9515	14657	1.1	3.0E-72	AF143892.1	NT	Homo sapiens thiorodotin-like protein (TXNL) gene, exon 3
4518	9338	14781	2.83	3.0E-72	11416198	NT	Homo sapiens thiorodotin-like protein (FLJ11127), mRNA
4732	9845	14990	1.34	3.0E-72	AF167572.1	NT	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds
4732	9845	14991	1.34	3.0E-72	AF167572.1	NT	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds
4889	10010	15185	1.06	3.0E-72	AI664337.1	EST_HUMAN	W831e08.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2307284 3'
2067	7183	12423	1.08	1.0E-72	AA948225.1	EST_HUMAN	ab3402.x1 Scores_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1387395 3'
1472	6599	11785	1.63	9.0E-73	AW374988.1	EST_HUMAN	MRO-CT0063-071089-002-ht1 CT0063 Homo sapiens cDNA
1040	6180	11345	1.57	8.0E-73	AW071795.1	EST_HUMAN	ws55606.x1 NCI CGAP Bm25 Homo sapiens cDNA clone IMAGE:2501088 3' similar to TRQ58050
1428	6555	11737	2.38	8.0E-73	AO24877.1	EST_HUMAN	Q69050 HYPOTHETICAL PROTEIN MJ1656 ;
1135	6272	11436	1.92	7.0E-73	8823280	NT	ov39h08.x1 Scores_basile_NHT Homo sapiens cDNA clone IMAGE:1639743 3'
							Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA

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Table 4

Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3293	8432	13594	0.89	7.0E-73	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
4921	10031		1.81	7.0E-73	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C082
163	5350		2.16	6.0E-73	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
1348	6475	11855	2.17	3.0E-73	AW843789.1	EST_HUMAN	CMD-CN0044-260100-164-08 CN0044 Homo sapiens cDNA
1873	6883	12218	1.47	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
1873	6883	12218	1.47	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
852	6003	11174	2.63	2.0E-73	AF138897.1	NT	Homo sapiens BASST (BASS1) mRNA, partial cds
1950	7088		3.28	2.0E-73	AW888081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
2271	7381		1.06	2.0E-73	U01371.1	NT	Human beta globin region on chromosome 11
3181	6312	13473	3.88	2.0E-73	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3537	6879	13840	0.63	2.0E-73	7689539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
3537	8879	13841	0.63	2.0E-73	7689539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
4411	9531		1.08	2.0E-73	AL163293.2	NT	Homo sapiens chromosome 21 segment HS21C083
1783	6919	12129	2.37	1.0E-73	AU121585.1	EST_HUMAN	AU121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000480 5'
2458	7582	12814	1.05	1.0E-73	AF188349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
739	5895	11047	2.05	8.0E-74	4557428	NT	Homo sapiens CD39-like 4 (CD39L4) mRNA
1953	7070	12284	2.19	7.0E-74	AJ007689.1	NT	Homo sapiens NKGDZ gene, exon 10
3309	8458	13818	1.22	7.0E-74	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1123	8281	11428	3.46	6.0E-74	AF108907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
2294	7403	12654	89.23	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603453 5'
2294	7403	12655	89.23	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603453 5'
2827	7882	13144	1.2	6.0E-74	AW014039.1	EST_HUMAN	UHH-B10-eat-h-03-0-U1.e1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709385 3'
2827	7882	13146	1.2	6.0E-74	AW014039.1	EST_HUMAN	UHH-B10-eat-h-03-0-U1.e1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709385 3'
3692	8930	13984	1.39	6.0E-74	BE048848.1	EST_HUMAN	h84e1.1 x1 NCL_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3132332 3'
3692	8930	13985	1.39	6.0E-74	BE048848.1	EST_HUMAN	h84e1.1 x1 NCL_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3132332 3'
5011	10114	15244	1	6.0E-74	4758135	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S cerevisiae CHL1-like helicase) (DDX11) mRNA
5011	10114	15245	1	6.0E-74	4758135	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S cerevisiae CHL1-like helicase) (DDX11) mRNA
808	6058	11225	2.51	5.0E-74	AW020988.1	EST_HUMAN	df17c08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'
2693	7769		6.84	6.0E-74	AW382766.1	EST_HUMAN	PMD-CT0289-271089-001-H07 CT0289 Homo sapiens cDNA

Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
277	5468	10609	5.66	4.0E-74	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
853	6004	11175	11.32	4.0E-74	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
1888	7083	12307	1.19	4.0E-74	AB028998.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1866	7083	12308	1.19	4.0E-74	AB028998.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2084	7180	12419	11.24	4.0E-74	4506182	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2084	7160	12420	11.24	4.0E-74	4506182	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2123	7238	12481	1.98	4.0E-74	AB032894.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2404	7510	12760	7.16	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene
3063	8216	13370	0.64	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene
3514	8555	13821	0.83	4.0E-74	AL183210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4038	9169	14310	1	4.0E-74	AL183247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4530	9848	14784	1.71	4.0E-74	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
4586	8704	14842	0.87	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
5057	10159	15280	1.18	4.0E-74	4604328	NT	Homo sapiens hydroxacyl-Coenzyme A dehydrogenase/3-ketacyl-Coenzyme A thiolase/Coenzyme A hydratase (bifunctional protein), beta subunit (HADHB) mRNA
5057	10159	15281	1.18	4.0E-74	4604328	NT	Homo sapiens hydroxacyl-Coenzyme A dehydrogenase/3-ketacyl-Coenzyme A thiolase/Coenzyme A hydratase (bifunctional protein), beta subunit (HADHB) mRNA
958	8107	11276	397.42	2.0E-74	7689491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
859	8107	11277	397.42	2.0E-74	7689491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1177	8312	11480	1.04	2.0E-74	AF020092.1	NT	Human endogenous retrovirus HERV-K-T47D
1248	8378	11557	3.01	2.0E-74	AI950528.1	EST_HUMAN	vs51e07 x1 NC1 CGAP_L128 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN
1608	8738	11929	3.81	2.0E-74	4885188	NT	Q08379 GOLGIN-95, contains element MER22 repetitive element;
1608	8738	11929	3.81	2.0E-74	4885188	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastitis leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
1608	8738	11930	3.81	2.0E-74	4885188	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastitis leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
2566	7867	12822	7.73	2.0E-74	AI557280.1	EST_HUMAN	PT2.1_15_G11.7 tumor2 Homo sapiens cDNA 3'
4993	10099	15229	2.72	2.0E-74	AL355082.1	NT	Novel human gene mapping to chromosome 22
4993	10099	15230	2.72	2.0E-74	AL355082.1	NT	Novel human gene mapping to chromosome 22
52	5264	10391	2.55	1.0E-74	7657354	NT	Homo sapiens Mismatch/NIK-related Kinase (MINK), mRNA
335	5518	10554	3.25	1.0E-74	AW818405.1	EST_HUMAN	QV4-ST0234-181189-037-005 ST0234 Homo sapiens cDNA
499	5666	10801	1.38	1.0E-74	8922828	NT	Homo sapiens hypothetical protein FLJ11028 (FLJ11028), mRNA

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
508	5872	10808	13.77	1.0E-74	X02344.1	NT	Homo sapiens beta 2 gene
598	5761	10889	1.72	1.0E-74	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
1000	6146	11313	2.39	1.0E-74	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C046
2208	7320	12571	3.67	1.0E-74	AB002068.1	NT	Homo sapiens DNA for Human P2XM, complete cds
3117	8269	13425	3.47	1.0E-74	4758637	NT	Homo sapiens marnosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
3895	9031	14180	0.87	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3895	9031	14191	0.87	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3941	9077	14231	6.64	1.0E-74	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4039	9170	14311	0.8	1.0E-74	BE983080.1	EST_HUMAN	RC3-BT0642-270300-019-06 BT0642 Homo sapiens cDNA
4241	9368	14489	0.72	1.0E-74	BE467789.1	EST_HUMAN	h273h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213683 3' similar to WP:B0511.12
2607	7708		2.28	8.0E-75	AF176228.1	NT	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
2289	7408	12689	1.55	6.0E-75	AI017416.1	EST_HUMAN	wk3a08.x1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:2417654 3' similar to gb:M14123_cds4
108	5312	10481	1.9	4.0E-75	BE081333.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN (HUMAN);
458	5628		1.35	4.0E-75	N36767.1	EST_HUMAN	QV1-BT0632-210200-079-02 BT0632 Homo sapiens cDNA
1778	6902	12110	1.14	4.0E-75	AW897230.1	EST_HUMAN	y60h08.r1 Soares melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:269055 5'
2811	7897	13127	6.48	4.0E-75	BE409464.1	EST_HUMAN	CMO-NN0057-150400-335-a11 NN0057 Homo sapiens cDNA
3483	8824	13791	1.18	4.0E-75	8922637	NT	601303868F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3683844 5'
1003	9149	11316	3.28	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1004	8149	11316	2.31	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1850	6971	12192	1.97	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
2400	7608	12766	2.07	3.0E-75	4758163	NT	Homo sapiens synaptonemal-associated protein, 20kD (SNAP29) mRNA
2893	8148	13308	0.81	3.0E-75	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3172	8323	13484	1.18	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
3332	8478	13842	0.65	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3332	8478	13843	0.65	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4139	9287	14407	1.34	3.0E-75	D81676.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4414	9634	14873	1.22	3.0E-75	7682421	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
2278	7388	12638	15.13	1.0E-75	AW108135.1	EST_HUMAN	xg00b02.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632707 3' similar to contains PTR7.1
2912	8088	13239	3.84	1.0E-75	X52221.1	NT	PT77 repetitive element;
43	5255	10375	7.93	9.0E-76	AI852848.1	EST_HUMAN	H.sapiens ERCC2 gene, exons 1 & 2 (partial)
							wb30b10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O76235 O76235
							TRAP1;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
43	5255	10376	7.83	8.0E-76	AI652848.1	EST_HUMAN	wk30b10.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:076235 076236
838	6086	11253	0.77	8.0E-76	4504374	NT	TRAP1;
838	6086	11254	0.77	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
							Homo sapiens H factor 1 (complement) (HF1) mRNA
778	5930	11089	2.91	7.0E-76	5016082	NT	Homo sapiens dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-
3276	8426	13686	2.56	7.0E-76	AF056490.1	NT	glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
3282	8431	13693	6.25	7.0E-76	4505052	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4360	9472	14609	4.76	7.0E-76	4507184	NT	Homo sapiens lymphocyte antigen 76 (LY76) mRNA, and translated products
4360	9472	14610	4.76	7.0E-76	4507184	NT	Homo sapiens septaplatin reductase (7- β -dihydroxypteridin:NADP+ oxidoreductase) (SPR) mRNA
1237	6367		72.97	8.0E-76	BE3366253.1	EST_HUMAN	Homo sapiens septaplatin reductase (7- β -dihydroxypteridin:NADP+ oxidoreductase) (SPR) mRNA
1947	7065	12288	28.9	5.0E-76	D63874.1	NT	601312018F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658757 5'
1947	7065	12289	28.9	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1947	7065	12290	28.9	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
628	6788	10920	1.68	3.0E-76	BF316282.1	EST_HUMAN	U1H-BW1-anz-b-04-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
628	6788	10921	1.68	3.0E-76	BF316282.1	EST_HUMAN	U1H-BW1-anz-b-04-0-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
1812	6740	11934	11.26	3.0E-76	4503478	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1812	6740	11935	11.26	3.0E-76	4503478	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3410	8553	13711	5.9	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
3410	8553	13712	5.9	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
							RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
4066	9185	14327	1.33	3.0E-76	BE348693.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
278	6468	10611	1.59	2.0E-76	D84285.1	NT	KIAA0782 PROTEIN ;
340	5523	10658	2.51	2.0E-76	D84285.1	NT	Human mRNA for possible protein TPRDII, complete cds
340	5523	10659	2.51	2.0E-76	D84285.1	NT	Human mRNA for possible protein TPRDII, complete cds
460	5628		1.09	2.0E-76	4557662	NT	Human mRNA for possible protein TPRDII, complete cds
588	5750	10878	2.7	2.0E-76	4503944	NT	Human sapiens immunoglobulin (IG) binding protein 1 (IGBP1) mRNA
1032	6173	11341	1.89	2.0E-76	4758053	NT	Homo sapiens glucagon (GCG) mRNA
1550	6878	11866	1.85	2.0E-76	4504028	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1550	6878	11869	1.85	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
2804	7860	13123	1.86	2.0E-76	P23266	SWISSPROT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
							OLFACTORY RECEPTOR-LIKE PROTEIN F8
3279	8428	13590	2.04	2.0E-76	AA445992.1	EST_HUMAN	z664602.s1 Soares_bastis_NHT Homo sapiens cDNA clone IMAGE:780988 3' similar to SW:ITB5_HUMAN
							P18084 INTEGRIN BETA-6 SUBUNIT PRECURSOR ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3278	8428	13391	2.04	2.0E-76	AA445992.1	EST_HUMAN	zu64e02.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:780888 3' similar to SW:ITB5_HUMAN P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR. ;
3749	8888	14037	0.8	2.0E-76	AA400700.1	EST_HUMAN	zu70g111.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:748398 5' similar to WP:R05D3.2 CE00281 ;
4108	5488	10811	1.33	2.0E-76	D84285.1	NT	Human mRNA for possible protein TPRDII, complete cds
4825	10035	15178	5.85	2.0E-76	AW878818.1	EST_HUMAN	QV9-O10028-220300-132-b11 OT0028 Homo sapiens cDNA
4273	8397	14638	4.94	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
4273	8397	14637	4.94	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
183	6377	10518	4.2	8.0E-77	R83144.1	EST_HUMAN	Yp11h02.r1 Scores_breast 3NDR-Hst Homo sapiens cDNA clone IMAGE:187165 5' similar to SP:ANKB_HUMAN C01484 ANKYRIN, BRAIN VARIANT 1 ;
4498	9615	14766	1.32	8.0E-77	BF205181.1	EST_HUMAN	601868828F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4108603 5'
1904	7053	12275	1.51	7.0E-77	AA825753.1	EST_HUMAN	zu81g01.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
2388	7494	12747	8.1	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kd) (POLR2E) mRNA
2388	7494	12748	8.1	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kd) (POLR2E) mRNA
280	6450	10589	3.18	6.0E-77	4504600	NT	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
1143	6280	11444	1.27	6.0E-77	AW95753.1	EST_HUMAN	EST368823 MAGE resequences, MAGE Homo sapiens cDNA
1597	6688	11874	2.81	6.0E-77	AI204086.1	EST_HUMAN	ge77h12.x1 Scores_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1745083 3'
1239	8388	11542	1.81	5.0E-77	AF041015.1	NT	7 Homo sapiens glucokinase (GCK) gene, exon 2
1369	6497	11680	2.47	5.0E-77	4957250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2648	7744	12897	2.88	5.0E-77	AF162668.1	NT	Homo sapiens tousel-like kinase 1 (TLK1) mRNA, complete cds
2725	7820	13075	2.78	5.0E-77	4503160	NT	Homo sapiens cullin 1 (CUL1) mRNA
3508	8849	13816	1.22	5.0E-77	8394518	NT	Homo sapiens ubiquitin specific protease 18 (USP18), mRNA
4913	10223	15187	2.57	5.0E-77	AL043953.1	EST_HUMAN	DKFZp434G1728.r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G1728 5'
3678	8817	13974	1.05	4.0E-77	AL449788.1	EST_HUMAN	AL449788 Homo sapiens fetal brain (Stavrides GS) Homo sapiens cDNA
1874	7091	12320	1.58	3.0E-77	6730038	NT	Homo sapiens SET domain and maf-like transcription factor gene (SETMAR) mRNA
1874	7091	12321	1.58	3.0E-77	6730038	NT	Homo sapiens SET domain and maf-like transcription factor gene (SETMAR) mRNA
1369	6488	11688	2.58	2.0E-77	AV784817	EST_HUMAN	AV784817 MDS Homo sapiens cDNA clone MDSBTF10 5'
1442	6570	11757	8.94	2.0E-77	AW897712.1	EST_HUMAN	RC3-BN0053-170200-011-101 BN0053 Homo sapiens cDNA
2094	7209	12456	2.55	2.0E-77	7708315	NT	Homo sapiens CGP-79 protein (LOC51634), mRNA
2558	7643	12610	3.88	2.0E-77	AB037838.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2558	7643	12611	3.88	2.0E-77	AB037838.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
4008	9139	14280	2.08	2.0E-77	BE044318.1	EST_HUMAN	hs43b05.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2_HUMAN P10264 RETROVIRUS-RELATED GAG POLYPROTEIN ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4390	9510	14852	0.8	2.0E-77	AI813519.1	EST_HUMAN	W22902.X1 NCL_CGAP_Bri52 Homo sapiens cDNA clone IMAGE:280468 3' similar to TR:O68245 O65245 F21E10.7 PROTEIN ;
4390	9510	14853	0.8	2.0E-77	AI813519.1	EST_HUMAN	W22902.X1 NCL_CGAP_Bri52 Homo sapiens cDNA clone IMAGE:280468 3' similar to TR:O68245 O65245 F21E10.7 PROTEIN ;
4569	9987		1.29	2.0E-77	4504098	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
4794	9947	14993	3.28	2.0E-77	AA853025.1	EST_HUMAN	ns88g12.s1 NCL_CGAP_Py2 Homo sapiens cDNA clone IMAGE:1189838 similar to SW:RL28_HUMAN P47914 603 RIBOSOMAL PROTEIN L29. [1] contains element MSR1 repetitive element ;
42	5253	10371	0.91	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
42	5253	10372	0.91	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
270	5460	10600	3.44	1.0E-77	4502188	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
270	5460	10601	3.44	1.0E-77	4502188	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
876	7903	11189	5.88	1.0E-77	4502188	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
876	7903	11200	5.89	1.0E-77	4502188	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1922	7041	12262	2.1	1.0E-77	AW058119.1	EST_HUMAN	w83e05.X1 Scanes_Tymus_NHITn Homo sapiens cDNA clone IMAGE:2536180 3'
2421	7628	12779	1.28	1.0E-77	AB029024.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
3017	9171	13327	2.24	1.0E-77	4503300	NT	Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DEOR1), mRNA
4330	8452	14586	3.21	1.0E-77	7706299	NT	Homo sapiens CGI-80 protein (LOC51626), mRNA
4488	9617	14758	17.87	1.0E-77	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4619	9737	14875	1.92	1.0E-77	8552322	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA
4682	9778	14822	1.8	1.0E-77	AJ273014.1	EST_HUMAN	q08g04.X1 NCL_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1981110 3'
4851	9963	15108	1.07	1.0E-77	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
4944	9695	14734	0.87	1.0E-77	4768053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
5051	10153	15284	1.49	1.0E-77	7681849	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
5051	10153	15285	1.48	1.0E-77	7681849	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
82	5291	10431	1.88	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
82	5291	10432	1.88	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
215	5409	10549	1.15	5.0E-78	11422488	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2631	7634	12882	4.52	5.0E-78	AW673424.1	EST_HUMAN	b54h03_x3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800405 5' similar to WP:Y4896A.6
3368	8511	13678	3.9	5.0E-78	M55586.1	NT	CE22121 ; Human collagenase type IV (CLG4) gene, exon 6
1138	6275	11439	1.7	4.0E-78	AL043314.2	EST_HUMAN	DKFZp434N0323_1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434N0323 5'
1533	6850	11846	1.38	4.0E-78	AL355841.1	NT	Novel human gene mapping to chromosome 22
1661	6789	11894	1.52	4.0E-78	AL865094.1	EST_HUMAN	w97b12x1 NCLCGAP_Kid11 Homo sapiens cDNA clone IMAGE:2486616 3' similar to SW:WAP_PIG O46555 WHEY ACIDIC PROTEIN PRECURSOR ;
2296	7405	12857	22.41	4.0E-78	AF107405.1	NT	Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
4299	8421	14663	1.52	4.0E-78	7638878	NT	Homo sapiens synovial (LOC30816), mRNA
4740	8853	14939	1.57	4.0E-78	4505809	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4740	8853	15000	1.57	4.0E-78	4505809	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
158	5353	10492	2.72	3.0E-78	AF095801.1	NT	Homo sapiens eRF1 gene, complete cds
158	5353	10493	2.72	3.0E-78	AF095801.1	NT	Homo sapiens eRF1 gene, complete cds
2278	7369	12639	1.84	3.0E-78	4502142	NT	Homo sapiens apoptosis inhibitor 3 (API3) mRNA
2393	7499	12750	1.98	3.0E-78	7708705	NT	Homo sapiens SHS and PX domain-containing protein SH-SPX1 (SH-SPX1), mRNA
3189	8350	13513	0.95	3.0E-78	4507184	NT	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
3744	8882		1.86	3.0E-78	AU140604.1	EST_HUMAN	AU140604 PLACE3 Homo sapiens cDNA clone PLACE3000373 5'
3783	8930	14078	0.74	3.0E-78	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
4080	8930	14078	0.82	3.0E-78	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
3098	8261		2.33	2.0E-78	U04489.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
3089	9123	14627	1.51	2.0E-78	AA311872.1	EST_HUMAN	EST182583 Jurkat T-cells VI Homo sapiens cDNA 5' end
4687	9783	14627	3.72	9.0E-79	11525891	NT	Homo sapiens peptide YY (PYY), mRNA
4833	9945	15088	3.54	9.0E-79	BE000837.1	EST_HUMAN	RC2-BN0074-090300-014-c12 BN0074 Homo sapiens cDNA
3723	8861	14014	1.12	8.0E-79	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4468	9587	14725	1.44	8.0E-79	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
4468	9587	14726	1.44	8.0E-79	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
5128	10228	15363	0.87	8.0E-79	8567387	NT	Homo sapiens perid (Drosophila) homolog 3 (PER3), mRNA
3235	8385	13647	11.83	7.0E-79	BE316848.1	EST_HUMAN	801472766T1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3876657 3'
3165	8307		1.45	4.0E-79	8622325	NT	Homo sapiens hypothetical protein FLJ10283 (FLJ10283), mRNA
311	5497	10637	1.08	3.0E-79	AF114488.1	NT	Homo sapiens interseitin short isoform (ITSN) mRNA, complete cds
978	6125	11256	3.13	3.0E-79	AF232708.1	NT	Homo sapiens cell-line tsA201a chloride ion current inducer protein I(Cn) gene, complete cds
3072	8226	13376	1.84	3.0E-79	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
285	8474		0.82	2.0E-79	H63128.1	EST_HUMAN	y48f03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208641 3'
633	5704	10928	1.36	2.0E-79	BE378928.1	EST_HUMAN	601169415F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:351107 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
928	6077	11248	2.08	2.0E-79	4757841	NT	Homo sapiens BCL2-like 2 (BCL2L2) mRNA
1037	6178		0.89	2.0E-79	AI623747.1	EST_HUMAN	th18h07.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2118885 3'
1789	6924	12134	0.97	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA
1789	6924	12135	0.97	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4), mRNA
1898	7006	12226	2	2.0E-79	7662265	NT	Homo sapiens KIAA0703 gene product (KIAA0703), mRNA
2132	7248	12400	5.6	2.0E-79	4585883	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2132	7248	12491	5.6	2.0E-79	4585883	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2176	7289	12636	2.64	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
2291	7400	12653	8.4	2.0E-79	AF244138.1	NT	Homo sapiens hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cds
2846	7648	12897	2.34	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
2846	7648	12898	2.34	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
2877	7774	13025	1.18	2.0E-79	AB023154.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
4138	9284	14403	1.27	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
5197	10294	15431	1.23	2.0E-79	11421885	NT	Homo sapiens sodium calcium exchanger (NCKX3), mRNA
3124	8276	13431	7.56	9.0E-80	AA725948.1	EST_HUMAN	al23e05.e1 Soares_testis NHT Homo sapiens cDNA clone 1343848 3'
3124	8276	13432	7.66	9.0E-80	AA725948.1	EST_HUMAN	al23e05.e1 Soares_testis NHT Homo sapiens cDNA clone 1343848 3'
3887	8727		1.21	8.0E-80	U94387.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
4934	10044	15184	1.07	7.0E-80	H04919.1	EST_HUMAN	Y49d02.r1 Soares_pleocenta Nb2HP Homo sapiens cDNA clone IMAGE:152087 5'
901	6051	11221	2.38	6.0E-80	AI422197.1	EST_HUMAN	tf58d02.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUJEM_HUMAN
1855	6783	11976	2.63	6.0E-80	U64808.1	NT	Q16785 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;
2272	7382	12629	3.33	6.0E-80	6831084	NT	Homo sapiens NRD convertase mRNA, complete cds
2272	7382	12630	3.33	6.0E-80	6831084	NT	Homo sapiens NRD convertase maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
4259	9384	14519	1.06	6.0E-80	AB032981.1	NT	Homo sapiens maintenance of telomeres maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
4259	9384	14520	1.05	6.0E-80	AB032981.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
598	5748	10877	34.63	5.0E-80	4508228	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
838	5988	11156	2.08	5.0E-80	AF108830.1	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA
838	5988	11167	2.08	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
1191	6325		0.97	5.0E-80	X91647.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
1488	6595		1.14	5.0E-80	AL163283.2	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
2341	7448	12702	1.26	5.0E-80	U89358.1	NT	H. sapiens ncd1 gene (exon 12)
2408	7514	12764	1.88	5.0E-80	AB037855.1	NT	Homo sapiens chromosome 21 segment H321C083
						NT	Human K31mt protein homolog mRNA, complete cds
						NT	Homo sapiens mRNA for KIAA1434 protein, partial cds

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Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2755	7849	13104	8.65	5.0E-80	4504282	NT	Homo sapiens H3 histone family, member J (H3FJ) mRNA
4013	9146	14287	0.97	5.0E-80	AB018038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4013	9146	14288	0.97	5.0E-80	AB018038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4833	10043	15183	1.32	5.0E-80	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
214	6408		10.59	3.0E-80	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4878	9782	14838	1.3	3.0E-80	BF085009.1	EST_HUMAN	PMO-GN0018-040500-002-E03 GN0018 Homo sapiens cDNA
4883	9894		3.62	3.0E-80	BE817466.1	EST_HUMAN	QV4-BN0263-040600-241-g10 BN0263 Homo sapiens cDNA
1810	6833	12148	3.63	2.0E-80	R35321.1	EST_HUMAN	Y655a08.f1 Scanes Infant brain (NIB) Homo sapiens cDNA clone IMAGE:38060 5'
1871	6891	12216	3.99	2.0E-80	AI444821.1	EST_HUMAN	RET487 subtracted ratna cDNA library Homo sapiens cDNA clone RET487
2047	7163	12402	15.22	2.0E-80	AL043118.2	EST_HUMAN	DKFZp434D1323_f1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434D1323 5'
338	5521		1.4	1.0E-80	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
800	5854	11114	1.88	1.0E-80	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1858	7075		1.44	1.0E-80	A1732856.1	EST_HUMAN	nm011212.x5 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:1078495 3' similar to contains OFFL1 ORF
4440	8559	14701	1.01	1.0E-80	AF071188.1	NT	repetitive element;
5111	10212	15349	1.01	1.0E-80	4557810	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
4368	9487	14630	6.13	6.0E-81	BE266829.1	EST_HUMAN	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
4368	9487	14631	5.13	6.0E-81	BE266829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3362840 5'
2169	7911	12683	7.48	6.0E-81	BE268042.1	EST_HUMAN	60111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3362840 5'
218	5412	10551	0.61	4.0E-81	AF252257.1	NT	Homo sapiens CRP2 binding protein mRNA, partial cds
700	5857	11005	1.37	4.0E-81	AI521435.1	EST_HUMAN	h000e12.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2122702 3' similar to TR:Q85560 Q85560
1833	6956	12178	1.73	4.0E-81	AW776812.1	EST_HUMAN	h088d02.x1 NCL CGAP_Cot14 Homo sapiens cDNA clone IMAGE:3035807 3' similar to SW:COFG_BOVIN
3150	8301	13481	3.42	4.0E-81	AB037768.1	NT	P83620 COATOMER GAMMA SUBUNIT ;
3908	8747	13503	0.89	4.0E-81	AW004608.1	EST_HUMAN	Homo sapiens mRNA for KIAA1345 protein, partial cds
4132	9250	14397	2.2	4.0E-81	AF263308.1	NT	w890h03.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2505289 3' similar to TR:Q43815 Q43815
4132	9250	14398	2.2	4.0E-81	AF263308.1	NT	STRATIN ;
1271	6400	11572	10.35	3.0E-81	Y18000.1	NT	Homo sapiens reb3 interacting protein variant 2 mRNA, partial cds
1271	6400	11573	10.35	3.0E-81	Y18000.1	NT	Homo sapiens reb3 interacting protein variant 2 mRNA, partial cds
2351	7458	12713	4.34	3.0E-81	AF077188.1	NT	Homo sapiens NF2 gene
2660	8114	13276	5.69	3.0E-81	4506280	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
							Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2680	8114	13277	5.89	3.0E-81	4506280	NT	Homo sapiens platelet-derived growth factor 8, neurite growth-promoting factor 1 (PTN) mRNA
2784	7651	13118	2.9	2.0E-81	BE784638.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
2784	7651	13117	2.9	2.0E-81	BE784638.1	EST_HUMAN	601474072F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3877121 5'
3784	8891	14042	0.8	2.0E-81	AW611542.1	EST_HUMAN	h985001.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952384 3'
1431	6528	11741	1.19	1.0E-81	W28639.1	EST_HUMAN	3333 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4489	9608	14748	3.07	1.0E-81	AA040370.1	EST_HUMAN	z44509.1 Soares_pregnant_uterus_NIHPU Homo sapiens cDNA clone IMAGE:465925 5' similar to
4614	9732	14899	6.85	1.0E-81	BE047998.1	EST_HUMAN	PIR-S62437 S62437 CDP-diacylglycerol synthase - fruit fly;
12	5223	10335	6.88	8.0E-82	AF161403.1	NT	bx45c04.y1 NCI CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2281628 5'
103	5223	10335	3.89	8.0E-82	AF161403.1	NT	Homo sapiens HSPC288 mRNA, partial cds
261	5451	10590	3.03	8.0E-82	U09988.1	NT	Homo sapiens CRFB4 gene, partial cds
815	5938	11128	2.28	8.0E-82	U09988.1	NT	Homo sapiens CRFB4 gene, partial cds
888	6038	11209	1.2	8.0E-82	U09988.1	NT	Human CRFB4 gene, partial cds
1501	6628	11816	1.33	8.0E-82	AB037748.1	NT	Human CRFB4 gene, partial cds
1870	6799	11895	1.21	8.0E-82	6715601	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
4222	9347	14480	0.71	8.0E-82	8823432	NT	Homo sapiens glutathione peroxidase 5 (epitidymal androgen-related protein) (GPX5), transcript variant 2, mRNA
1463	6590		1.1	7.0E-82	BF035327.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA
2728	7823	13078	1.6	7.0E-82	AU144050.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882088 5'
1685	6814	12012	61.3	4.0E-82	AF081484.1	NT	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000752 3'
275	5485	10807	14.66	3.0E-82		NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
701	5858	11008	2.28	3.0E-82	BE006706.1	EST_HUMAN	Homo sapiens amyloid beta (A4) precursor protein (precursor protein (precursor protein) (APP), mRNA
788	5942	11102	8.05	3.0E-82	5174702	NT	RC2-BN0120-010400-013-002 BN0120 Homo sapiens cDNA
871	6022	11183	8.74	3.0E-82	4502168	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
1082	6203		63.03	3.0E-82	AA725848.1	EST_HUMAN	Homo sapiens amyloid beta (A4) precursor protein (precursor protein (precursor protein) (APP), mRNA
1382	6401	11673	1.14	3.0E-82	AW875073.1	EST_HUMAN	al23905.81 Soares_tests_NHT Homo sapiens cDNA clone 1343848 3'
1478	6506	11791	2.92	3.0E-82	AL163295.2	NT	RC8-PT0001-100100-021-B02 PT0001 Homo sapiens cDNA
1907	7028	12246	1.31	3.0E-82	BE813232.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C085
3265	8405		1.94	3.0E-82	5453811	NT	RC1-BN0005-280700-018-g04 BN0005 Homo sapiens cDNA
695	5757	10884	1.4	2.0E-82	AB023218.1	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA
685	5787	10885	1.4	2.0E-82	AB023218.1	NT	Homo sapiens mRNA for KIAA0869 protein, partial cds
							Homo sapiens mRNA for KIAA0869 protein, partial cds

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Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1700	6828	12029	2.13	2.0E-82	AL046390.1	EST_HUMAN	DKFZp434M117.1 434 (synonym: hras3) Homo sapiens cDNA clone DKFZp434M117.5'
2948	8102	13207	0.7	2.0E-82	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3823	8059	14107	1	2.0E-82	D87876.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4212	8337	14470	0.88	2.0E-82	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4531	8949	14785	1.11	2.0E-82	AB028018.1	NT	Homo sapiens mRNA for KIAA1088 protein, partial cds
4531	8949	14786	1.11	2.0E-82	AB028018.1	NT	Homo sapiens mRNA for KIAA1088 protein, partial cds
4841	9853	15098	2.94	2.0E-82	AFO45555.1	NT	Homo sapiens wbc1 (WBSCR1) and wbc6 (WBSCR6) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
5064	10168	16289	1.42	2.0E-82	4607580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5064	10168	16300	1.42	2.0E-82	4607580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
590	5762	10879	1.35	1.0E-82	11545921	NT	Homo sapiens melanoma differentiation associated protein-9 (MDA9), mRNA
1211	6343	11592	1.88	1.0E-82	BE885108.1	EST_HUMAN	601510859F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE33912207 5'
1289	6418	11592	4.73	1.0E-82	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-F10 BT0310 Homo sapiens cDNA
1280	6418	11593	1.7	1.0E-82	AB011110.2	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
1421	6548	11729	3.25	8.0E-83	BE363973.1	EST_HUMAN	601275348F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE33614302 5'
1695	7871	12023	2.23	8.0E-83	N68951.1	EST_HUMAN	244812.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:285823 3'
1384	6493	11674	1.56	7.0E-83	AW385628.1	EST_HUMAN	QV4-LT0018-271289-068-h11 LT0018 Homo sapiens cDNA
2820	7884		1.62	7.0E-83	AA584655.1	EST_HUMAN	nc12h01.s1 NCI CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element
4784	9897		6.62	7.0E-83	BF221813.1	EST_HUMAN	7p37a07.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3647863 3' similar to TR-Q9Y318 Q9Y318 (LUBE2D3) genes, complete cds
403	5570	10717	1.49	6.0E-83	M35320.1	NT	Human platelet Glycoprotein Iib (GPIIb) gene, exons 2-29
1787	6922	12132	2.43	6.0E-83	AW573088.1	EST_HUMAN	fr31h03.x1 Soares NFL_I_GBC.S1 Homo sapiens cDNA clone IMAGE:2933525 3' similar to
3023	8177		0.83	6.0E-83	AF231018.1	NT	SW:Y8EB_HAEIN P4471 HYPOTHETICAL PROTEIN H10034. ;
3548	8889	13851	0.75	6.0E-83	11430241	NT	Homo sapiens chromosome 21 unknown mRNA
946	8094		1.51	5.0E-83	U17883.1	NT	Homo sapiens hypothetical protein FLJ10378 (FLJ10378), mRNA
2042	7878		8.24	5.0E-83	AFO06305.1	NT	Human eucalcin dehydrogenase iron-protein subunit (cdhB) gene, exon 6
3616	8753	13913	2.15	5.0E-83	AL133207.2	NT	Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds
3883	8019	14178	1.77	5.0E-83	4885160	NT	Novel human gene mapping to chromosome X
5062	10164	15297	11.94	5.0E-83	4657013	NT	Homo sapiens deoxyribonuclease I (DNASE1), mRNA
5062	10164	15298	11.94	5.0E-83	4657013	NT	Homo sapiens catallase (CAT) mRNA
639	5800	10934	1.69	4.0E-83	AF224683.1	NT	Homo sapiens marnosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds

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Single Exon Probes Expressed in BT474 Cells.

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
898	8144		3.26	3.0E-83	AA368311.1	EST_HUMAN	EST195422 Placenta 1 Homo sapiens cDNA similar to endogenous retrovirus ERV8
2738	7832		1.09	3.0E-83	AA632854.1	EST_HUMAN	np87c07.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133292 similar to contains THR12 THR repetitive element;
1812	6936	12160	2.11	2.0E-83	AA993492.1	EST_HUMAN	cd84g05.s1 Soares_bests_NHT Homo sapiens cDNA clone IMAGE:1621692 3' similar to TRCQ2814
1812	6936	12161	2.11	2.0E-83	AA993492.1	EST_HUMAN	cd84g05.s1 Soares_bests_NHT Homo sapiens cDNA clone IMAGE:1621692 3' similar to TRCQ2814
1930	7049	12270	2.01	2.0E-83	N68951.1	EST_HUMAN	z448f12.s1 Soares fetal liver spleen 1NPL3 Homo sapiens cDNA clone IMAGE:235823 3'
2162	7276	12522	0.97	2.0E-83	AB033088.1	NT	Homo sapiens mRNA for KIAA1272 protein, partial cds
2814	7970	13120	1.26	2.0E-83	BE286894.1	EST_HUMAN	RC8-ET0048-280900-013-H12 ET0048 Homo sapiens cDNA
3252	8402		1.97	2.0E-83	11430834	NT	Homo sapiens esi (Drosophila)-like 1 (SALL1), mRNA
3755	8892		0.7	2.0E-83	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4313	9435	14570	4.13	2.0E-83	AF202879.1	NT	Homo sapiens hematopoietic progenitor cell antigen CD34 precursor (CD34) mRNA, partial cds
4620	9738	14876	9.02	2.0E-83	7706398	NT	Homo sapiens enkyrin repeat-containing protein ASB-2 (LOC51676), mRNA
4620	9738	14877	9.02	2.0E-83	7706398	NT	Homo sapiens enkyrin repeat-containing protein ASB-2 (LOC51676), mRNA
1419	6546	11726	3.66	1.0E-83	4504326	NT	Homo sapiens hydroxycarboxyl-Coenzyme A dehydrogenase 3-ketacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1419	6546	11727	3.66	1.0E-83	4504326	NT	Homo sapiens hydroxycarboxyl-Coenzyme A dehydrogenase 3-ketacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
2817	7716	12970	4.89	1.0E-83	BE883880.1	EST_HUMAN	601507375F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3008754 5'
3163	8314	13476	0.93	1.0E-83	7662349	NT	Homo sapiens cell recognition molecule Casp2 (KIAA0888), mRNA
3847	8983	14138	7.16	1.0E-83	AF053788.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP80 mRNA, partial cds
4223	9348	14481	2.31	1.0E-83	Z25822.1	NT	H. sapiens gene for mitochondrial dodecanoyl-CoA dehydrogenase, exon 3
4857	9939	15114	1.56	1.0E-83	4502169	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3774	8911	14084	3.43	7.0E-84	BE901209.1	EST_HUMAN	60167623F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3968853 5'
1289	6428	11600	4.09	6.0E-84	BE938864.1	EST_HUMAN	RC2-FN0119-200500-011-g05 FN0119 Homo sapiens cDNA
1289	6428	11601	4.09	6.0E-84	BE938864.1	EST_HUMAN	RC2-FN0119-200500-011-g05 FN0119 Homo sapiens cDNA
2374	7480	12734	3.37	6.0E-84	AA776574.1	EST_HUMAN	ae8a03.s1 Siratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:971020 3'
712	8869	11017	0.8	5.0E-84	AA362811.1	EST_HUMAN	EST180994 Testis 1 Homo sapiens cDNA 5' end
2885	8139		1.7	6.0E-84	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1395	6573	11694	0.97	4.0E-84	AB037735.1	NT	Homo sapiens mRNA for KIAA1314 protein, partial cds
1418	6646	11729	3.03	4.0E-84	AI685321.1	EST_HUMAN	wa76c04.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2302088 3' similar to SW_NRDC_HUMAN 043847 NARDILYSIN PRECURSOR;

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4928	10038	15178	0.98	4.0E-84	4506928	NT	Homo sapiens polymerase (DNA-directed), alpha (70kD) (POLA2), mRNA
4929	10039	15179	1.84	4.0E-84	AF06901.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
5129	10228	15364	1.04	4.0E-84	AA401549.1	EST_HUMAN	z182a07.t1 Soares, testes_NHT Homo sapiens cDNA clone IMAGE:742548 5' similar to WP.F2286.1
314	5500	10840	1.87	3.0E-84	AF026200.1	NT	CE02185 GTP-BINDING ADP-RIBOSYLATION FACTOR;
1884	7081	12305	2.8	3.0E-84	5453855	NT	Homo sapiens Bach1 protein homolog mRNA, partial cds
2066	7123	12359	7.05	3.0E-84	AL096380.1	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
3730	8887	14021	8.04	3.0E-84	AF014469.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
2066	7211	12458	3.39	2.0E-84	BE695397.1	EST_HUMAN	Homo sapiens X-linked juvenile retinoschidia precursor protein (XLRSP) mRNA, complete cds
2066	7211	12459	3.39	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0785-180600-272-508 BT0785 Homo sapiens cDNA
2809	8053	13235	9.32	2.0E-84	AF036943.1	NT	CM1-BT0785-180600-272-508 BT0785 Homo sapiens cDNA
2831	8055	13252	1.4	2.0E-84	X68211.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1-L) mRNA, complete cds
4760	9873	15024	1.01	2.0E-84	BF306518.1	EST_HUMAN	H. sapiens DNA for endogenous retroviral like element
4760	9873	15025	1.01	2.0E-84	BF306518.1	EST_HUMAN	601887684F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121727 5'
310	5496	10636	1.31	1.0E-84	AF114488.1	NT	601887684F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121727 5'
548	5713	10847	54.29	1.0E-84	4507852	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
718	5878	11598	1.02	1.0E-84	11427631	NT	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA
1297	6426	11598	5.12	1.0E-84	AA984379.1	EST_HUMAN	Homo sapiens complement component 5 (C5), mRNA
2046	7182	12401	1.84	1.0E-84	BE382137.1	EST_HUMAN	am85b11.a1 Stratiotes echinops brain S11 Homo sapiens cDNA clone IMAGE:1623888 3'
2205	7317	12567	2.18	1.0E-84	11427197	NT	601306006F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626267 5'
3732	8870	14023	2.48	1.0E-84	AA720851.1	EST_HUMAN	Homo sapiens pericentriolar material 1 (PCM1), mRNA
4304	9514	14655	4.46	1.0E-84	AJ229041.1	NT	HW12803.s1 NCL_CGAP_SST1 Homo sapiens cDNA clone IMAGE:1239106 3'
4688	9784	14928	3.07	1.0E-84	AL043814.2	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4688	9784	14928	3.07	1.0E-84	AL043814.2	EST_HUMAN	DKFZp434N0323_11 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp434N0323 5'
4887	9514	14656	2.2	1.0E-84	AJ229041.1	NT	DKFZp434N0323_11 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp434N0323 5'
988	6115	11377	1.88	9.0E-85	AL163209.2	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
1074	6214	11378	7.67	9.0E-85	U51432.1	NT	Homo sapiens chromosome 21 segment HS21C009
1591	6720	11908	0.96	9.0E-85	M33282.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1591	6720	11910	0.98	9.0E-85	M33282.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1888	6817	12016	2.58	9.0E-85	7857020	NT	Human plasminogen gene, exon 7
4888	9999	15145	0.61	9.0E-85	AL163268.2	NT	Human plasminogen gene, exon 7
1137	6274	11438	8.3	7.0E-85	LD5094.1	NT	Homo sapiens DKFZp434P211 protein (DKFZp434P211), mRNA
							Homo sapiens chromosome 21 segment HS21C068
							Homo sapiens ribosomal protein L27 mRNA, complete cds

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Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2314	7422	12873	1.51	5.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1303	6433	11607	1.63	3.0E-85	AF088157.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6
1780	6916	12123	8.48	3.0E-85	T87495.1	EST_HUMAN	y63g09.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:121604 5'
4282	8414	14849	1.03	3.0E-85	BE207189.1	EST_HUMAN	601169704F2 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3533616 5'
4872	8983	15128	1.55	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4872	8983	15130	1.55	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
984	6111	11281	0.88	2.0E-85	7657288	NT	Homo sapiens KIAA0928 protein Mac2 interacting nuclear target (MINT) homolog (KIAA0928), mRNA
1042	6183	11349	3.03	2.0E-85	AF248540.1	NT	Homo sapiens interectin 2 (SH3D1B), mRNA, complete cds
1412	6339	11718	1.82	2.0E-85	7702205	NT	Homo sapiens CGI-201 protein (LOC51840), mRNA
1429	6356	11738	5.87	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2), mRNA
1429	6356	11739	5.87	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2), mRNA
2212	7324	12574	1.75	2.0E-85	U10625.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2783	8471		6.15	2.0E-85	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2894	8149	13309	1.39	2.0E-85	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4310	8432	14587	4.86	2.0E-85	4505880	NT	Homo sapiens plasminogen (PLG), mRNA
4888	8897	15143	0.99	2.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2263	7373		2.12	1.0E-85	BE794308.1	EST_HUMAN	601591418F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945818 5'
2370	7476	12730	4.1	1.0E-85	BE818392.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868021 5'
2370	7476	12731	4.1	1.0E-85	BE818392.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868021 5'
1436	6355		20.94	9.0E-86	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867690 5'
937	6085	11251	0.94	7.0E-86	AA860801.1	EST_HUMAN	g188108.g1 Soares parathyroid tumor_Nb1HPA Homo sapiens cDNA clone IMAGE:1403559 3'
837	6085	11252	0.94	7.0E-86	AA860801.1	EST_HUMAN	g188108.g1 Soares parathyroid tumor_Nb1HPA Homo sapiens cDNA clone IMAGE:1403559 3'
1288	6427	11599	4.98	6.0E-86	4505492	NT	Homo sapiens oxoglutarate dehydrogenase (liposomal) (OGDH), mRNA
208	5402	10548	3.94	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
4255	8390	14528	0.98	3.0E-86	BE867703.1	EST_HUMAN	601443262F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3847465 5'
204	5454	10592	1.31	2.0E-86	AA308284.1	EST_HUMAN	EST1177232 Jurkat T-cells VI Homo sapiens cDNA 5' end
413	5581		2.4	2.0E-86	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1192	6328	11453	1.68	2.0E-86	N58977.1	EST_HUMAN	y216a08.r1 Soares multiple sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:283478 5'
1505	6632	11818	1.43	2.0E-86	4759827	NT	Homo sapiens neuritin III (NRXN3), mRNA
1805	6632	11819	1.43	2.0E-86	4759827	NT	Homo sapiens neuritin III (NRXN3), mRNA
2174	7287	12535	1.05	2.0E-86	9835487	NT	Human endogenous retrovirus, complete genome
2249	7359	12818	3.27	2.0E-86	AB033103.1	NT	Homo sapiens mRNA for KIAA1277 protein, partial cds
3397	8541	13700	1.44	2.0E-86	AW568142.1	EST_HUMAN	EST1378215 IMAGE resequenced, MAGI Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3727	8884	14017	2.82	2.0E-88	AF159776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3727	8884	14018	2.82	2.0E-88	AF159776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
4014	9147		2.64	2.0E-88	AW516742.1	EST_HUMAN	h87g08.x1 NC1 CGAP G08 Homo sapiens cDNA clone IMAGE:2816642 3'
4766	9869	15019	2.51	2.0E-88	AF059490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 6A (PDE6A) mRNA, partial cds
5043	10145	15274	1.36	2.0E-88	4505778	NT	Homo sapiens phosphotyrosine kinase, alpha 1 (muscle) (PHKA1), mRNA
1610	6738	11932	2.76	1.0E-88	4826855	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75KD) (NADH-coenzyme Q reductase) (NDUFS1) mRNA
3141	8282	13449	1.36	1.0E-88	5463849	NT	Homo sapiens fibulin 5 (FBLN5) mRNA
3220	8371	13534	2.59	1.0E-88	L20492.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
3278	8427	13588	1.26	1.0E-88	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3278	8427	13589	1.26	1.0E-88	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3917	9053	14213	0.99	1.0E-88	7708181	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
3917	9053	14214	0.99	1.0E-88	7708181	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
4238	8963	14498	4.73	1.0E-88	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4896	10007	15152	1.27	1.0E-88	AF100751.1	NT	Homo sapiens FK506-binding protein FKBP23 isoform mRNA, complete cds
479	5848	10787	81.06	8.0E-87	X82246.1	NT	O cuticularis mRNA for elongation factor 1 alpha
3513	8654	13820	1.06	6.0E-87	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
5173	10270	15411	0.63	6.0E-87	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
1160	6288	11461	2.39	5.0E-87	AA382811.1	EST_HUMAN	ES-T86094 Testis I Homo sapiens cDNA 5' end
867	6114	11293	0.96	4.0E-87	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1174	6309	11476	18.49	4.0E-87	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1439	6566	11751	0.90	4.0E-87	R78133.1	EST_HUMAN	y80f10.J1 Soares placenta NB24-IP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element
2024	7141	12381	1	4.0E-87	AB007926.1	NT	Homo sapiens mRNA for KIAA0458 protein, partial cds
2389	7505	12763	1.48	4.0E-87	7706299	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
2389	7606	12764	1.48	4.0E-87	7706299	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
3446	8588	13761	1.76	4.0E-87	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) translocation) (MLL-T4) mRNA
2737	7831	13085	5.83	2.0E-87	4885420	NT	Homo sapiens high-mobility group (nonhistone chromosome) protein 4 (HMG4) mRNA
2914	8088		0.63	2.0E-87	BF327920.1	EST_HUMAN	QV0-BN0148-050860-264-a03 BN0148 Homo sapiens cDNA
3763	8900	14052	0.78	2.0E-87	AU116935.1	EST_HUMAN	AU116935 HEMBA1 Homo sapiens cDNA clone HEMBA1000307 5'
4889	10000	15146	0.6	2.0E-87	BF379311.1	EST_HUMAN	CMD-TN00338-150900-352-H08 TN00338 Homo sapiens cDNA
4941	10051	15189	1.37	2.0E-87	BE176476.1	EST_HUMAN	RC5-HT0580-200300-031-G04 HT0580 Homo sapiens cDNA
1184	7868		1.7	1.0E-87	7705693	NT	Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1441	6558	11753	1.93	1.0E-87	AW381977.1	EST_HUMAN	PM2-CT0265-141089-001-g04 CT0265 Homo sapiens cDNA
1441	6558	11754	1.93	1.0E-87	AW381977.1	EST_HUMAN	PM2-CT0265-141089-001-g04 CT0265 Homo sapiens cDNA
3688	8827	13982	12.69	1.0E-87	Y00082.1	NT	Human mRNA for T-cell cyclophilin
3715	8853	14007	2.88	1.0E-87	4759327	NT	Homo sapiens neuroxin III (NRXN3) mRNA
1107	8249	11408	0	9.0E-98	AF167485.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1358	6485	11685	2.83	9.0E-98	AB037820.1	NT	Homo sapiens mRNA for KIAA1398 protein, partial cds
1358	6485	11686	2.83	9.0E-98	AB037820.1	NT	Homo sapiens mRNA for KIAA1398 protein, partial cds
2111	7228	12468	1.12	9.0E-98	7681701	NT	Homo sapiens mRNA for KIAA1398 protein, partial cds
3607	8746	13902	1.03	9.0E-98	AL163209.2	NT	Homo sapiens DKFZP688P1622 protein (DKFZP688P1622), mRNA
4243	9368	14501	3.03	9.0E-98	X91929.1	NT	H. sapiens chromosome 21 segment HS21C009
4243	9368	14502	3.03	9.0E-98	X91929.1	NT	H. sapiens ECE-1 gene (exon 9)
4889	10095	15226	1.01	9.0E-98	AB026898.1	NT	H. sapiens ECE-1 gene (exon 9)
1842	6953		2.34	5.0E-98	7681887	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2803	7702	12959	9.44	5.0E-98	N88399.1	EST_HUMAN	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
2870	8124	13287	0.68	5.0E-98	AF114488.1	NT	K9719F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1
2882	8136	13300	0.63	5.0E-98	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
2882	8136	13301	0.63	5.0E-98	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
3370	8515		2.52	5.0E-98	AF68217.1	EST_HUMAN	w488h08.x1 NCL_OGAP_Lu24 Homo sapiens cDNA clone IMAGE2338799 3' similar to contains Alu repetitive element; contains element MER22 MER22 repetitive element ;
3523	8804	13851	0.87	5.0E-98	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
4705	9821	14958	0.62	5.0E-98	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
1334	6463	11843	1.8	4.0E-98	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
1334	6463	11844	1.8	4.0E-98	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
730	6886	11036	2.2	3.0E-98	11645800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
1824	6947		1.79	3.0E-98	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
2818	8087	13240	4.81	3.0E-98	N68851.1	EST_HUMAN	z448f12.s1 Scarsa fetal liver spleen 1NF18 Homo sapiens cDNA clone IMAGE255823 3'
4219	9344	14474	0.69	3.0E-98	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4219	9344	14475	0.69	3.0E-98	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4457	9676		3.97	3.0E-98	11429300	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
1038	6179	11343	1.32	2.0E-98	7305188	NT	Homo sapiens Calsenlin, presenilin-binding protein, EF hand transcription factor (CSENI), mRNA
1638	6765	11959	1.88	2.0E-98	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1782	6898	12094	4.8	2.0E-98	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4403	9523	14694	1.89	2.0E-88	5031660	NT	Homo sapiens dynein, axonemal, light polypeptide 4 (DNAH4), mRNA
2897	7793	13044	1.51	8.0E-89	BE311557.1	EST_HUMAN	601142400F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506188 5'
432	5001	10747	1.21	7.0E-88	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
432	5801	10748	1.21	7.0E-88	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
4853	6065	15110	3.03	7.0E-88	4557390	NT	Homo sapiens complement component 8, beta polypeptide (C8B), mRNA
4908	10018	16182	3.96	7.0E-89	AL046748.1	EST_HUMAN	DKFZp434E246_r1 434 (synonym: hncs3) Homo sapiens cDNA clone DKFZp434E246 5'
1024	6165	11331	1.26	6.0E-88	5903114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin), mRNA
2195	7507	12557	4.18	8.0E-88	4506124	NT	Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4), mRNA
2411	7517	12786	3.33	8.0E-88	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3), mRNA
2411	7517	12787	3.33	8.0E-88	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3), mRNA
3511	8582	13818	1.12	8.0E-88	7651817	NT	Homo sapiens HSPC169 protein (HSPC169), mRNA
4607	9725	14980	3.88	6.0E-89	AB007866.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
4607	9725	14981	3.88	6.0E-89	AB007866.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
5148	10248	15396	0.89	6.0E-89	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5148	10248	15397	0.89	6.0E-89	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5058	10160	15292	3	6.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCB8A Homo sapiens cDNA clone TCBAP0383
5058	10160	15293	3	6.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCB8A Homo sapiens cDNA clone TCBAP0383
2842	7897	13155	1.58	3.0E-89	AW976181.1	EST_HUMAN	EST388280 MAGe sequences, MAGN Homo sapiens cDNA
122	5575	10723	0.76	2.0E-89	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
122	5576	10724	0.76	2.0E-89	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
528	5694	10826	0.87	2.0E-89	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
2847	8002	13182	1.46	2.0E-89	AI222095.1	EST_HUMAN	q98608.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131
4118	9244	14380	1.49	2.0E-89	AF089897.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element
4125	9253	14391	6.06	2.0E-89	X58742.1	NT	H. sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4125	9253	14392	6.06	2.0E-89	X58742.1	NT	H. sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4326	9448	14581	1.08	2.0E-89	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4474	9583	14732	1.18	2.0E-89	AI007378.1	NT	Homo sapiens GGT gene, exon 5
1064	6205	11367	3.39	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1065	6205	11367	3.2	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1335	7914	11645	6.99	8.0E-90	BE070561.1	EST_HUMAN	7636f08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1335	7014	11648	8.99	8.0E-90	BE670561.1	EST_HUMAN	763608.x1 NCI_CGAP_LU24 Homo sapiens cDNA clone IMAGE:3284583 3'
837	5939		7	7.0E-90	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3040	8184	13349	1.25	6.0E-90	X91928.1	NT	H. sapiens ECE-1 gene (exon 6)
3040	8184	13350	1.25	6.0E-90	X91928.1	NT	H. sapiens ECE-1 gene (exon 6)
4204	8329	14481	7.5	6.0E-90	8022398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4204	8329	14482	7.6	6.0E-90	8022398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
150	6347		33.35	6.0E-90	AB035344.1	NT	Homo sapiens TCEB gene, exon 1-10b
1185	6328	11496	3.1	6.0E-90	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1831	6954	12176	1.41	6.0E-90	A1222095.1	EST_HUMAN	qg98c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSFERASE 1 PRECURSOR (HUMAN); contains Alu repetitive element
1831	6954	12176	1.41	6.0E-90	A1222095.1	EST_HUMAN	qg98c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSFERASE 1 PRECURSOR (HUMAN); contains Alu repetitive element
2525	7628	12876	1.38	6.0E-90	AF114487.1	NT	Homo sapiens intersectin long isoform (ITSN) mRNA, complete cds
4513	9631	14776	0.96	6.0E-90	4506354	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
4641	9759	14906	0.96	6.0E-90	AL135549.1	EST_HUMAN	DKFZ762P1616.1 762 (synonym: hmal2) Homo sapiens cDNA clone DKFZ762P1616 5'
300	5488	10629	2.48	4.0E-90	AF231620.1	NT	Homo sapiens chromosome 21 unknown mRNA
300	5488	10630	2.48	4.0E-90	AF231620.1	NT	Homo sapiens chromosome 21 unknown mRNA
1087	6225	11391	3.88	4.0E-90	4505316	NT	Homo sapiens gene encoding discoidin receptor subunit 1 (MYPT1), mRNA
1703	6831	12033	8.69	4.0E-90	X98033.1	NT	H. sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
2824	7860	13140	0.63	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2824	7860	13141	0.63	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2895	8150	13310	1.03	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2895	8150	13311	1.03	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4828	8744	14888	5.2	4.0E-90	D81675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4765	8879	15028	2.92	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4787	9800	15041	1.98	4.0E-90	M95887.1	NT	Human prothymosin converting enzyme (NEC2) gene, exon 8
211	5406	10548	3	2.0E-90	BE537913.1	EST_HUMAN	60106798F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453834 5'
1175	6310	11477	23.99	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1175	6310	11478	23.99	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
3822	8958	14108	1.81	2.0E-90	A1138213.1	EST_HUMAN	qg54c02.x1 Soares_placenta_8b9weeks_2N6HP8t9W Homo sapiens cDNA clone IMAGE:1713410 3' similar to SW:OLF3_MOUSE P23275 OLFACTORY RECEPTOR OR3.;

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4885	9856	15142	7.01	2.0E-60	5729855	NT	Homo sapiens GRB2-related adaptor protein (GRAP) mRNA
274	5464	10806	4.8	1.0E-60	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease novin-II, Alzheimer disease) (APP), mRNA
372	7863	10895	3.01	1.0E-60	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
373	7863	10896	2.12	1.0E-60	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
693	6850	10894	1.7	1.0E-60	AJ237689.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
693	6850	10895	1.7	1.0E-60	AJ237689.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
728	6884	11033	12.63	1.0E-60	AF264760.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
728	6884	11034	12.63	1.0E-60	AF264760.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1111	6249		4.98	1.0E-60	4507828	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA
1310	6440	11616	2.9	1.0E-60	AF098154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1310	6440	11617	2.9	1.0E-60	AF098154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1881	6810		5.61	1.0E-60	BE376884.1	EST_HUMAN	60115956372 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3611118 5'
1908	7027	12247	2.4	1.0E-60	11420514	NT	Homo sapiens similar to SALL1 (see Drosophila)-like (LOC57167), mRNA
2816	7872	13132	6.74	1.0E-60	6005720	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
3830	8968	14118	0.85	1.0E-60	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3830	8968	14119	0.85	1.0E-60	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
4401	9521	14682	1.31	1.0E-60	AF167340.1	NT	Homo sapiens soluble Interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 9 and complete cds, alternatively spliced
4168	9294	14432	5.3	8.0E-61	D12234.1	EST_HUMAN	HUM0005381 Liver HepG2 cell line. Homo sapiens cDNA clone c881 3'
1457	6584	11772	1.01	7.0E-61	AF063768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP80 mRNA, partial cds
3456	8598	13762	2.08	5.0E-61	AA702794.1	EST_HUMAN	zf80504.s1 Soares_fetal_liver_spleen_TNFSL_31 Homo sapiens cDNA clone IMAGE:448015 3'
4490	9609	14747	1.1	6.0E-61	AU143539.1	EST_HUMAN	AU143539 Y78AA1 Homo sapiens cDNA clone Y78AA1002087 5'
4490	9609	14748	1.1	6.0E-61	AU143539.1	EST_HUMAN	AU143539 Y78AA1 Homo sapiens cDNA clone Y78AA1002087 5'
4777	9880	15035	1.24	6.0E-61	7110834	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
4777	9880	15036	1.24	6.0E-61	7110834	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
3185	8836	13498	11.3	4.0E-61	AF166778.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3185	8836	13499	11.3	4.0E-61	AF166778.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
1629	6758	11952	2.26	3.0E-61		NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1629	6758	11953	2.26	3.0E-61		NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1802	7872	12140	1.36	3.0E-61	AF265555.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
3321	8468	13031	1.48	3.0E-61	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3444	8586	13748	2.88	3.0E-61	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3444	8586	13749	2.88	3.0E-61	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3767	8904	14057	2.29	3.0E-01	AF084530.1	NT	Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds
4984	8882	14821	3.8	3.0E-01	M30838.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4984	10072	15209	1.05	3.0E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4984	10072	15210	1.05	3.0E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
47	6269	10383	3.17	1.0E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1249	6379	11558	9.99	1.0E-01	AW449748.1	EST_HUMAN	UHH-B13-cto-4-01-0-U1.s1 NC1_CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2735280 3'
1245	6379	11552	10.34	9.0E-02	AJ001889.1	NT	Homo sapiens NKX2D gene, exon 10
1245	6379	11553	10.34	9.0E-02	AJ001889.1	NT	Homo sapiens NKX2D gene, exon 10
88	5287	10458	6.9	8.0E-02	W26367.1	EST_HUMAN	2833 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
283	5472	10814	6.48	8.0E-02	BE386363.1	EST_HUMAN	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614687 5'
5085	10185	15323	1.09	8.0E-02	AW157571.1	EST_HUMAN	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614687 5'
234	7886	10566	1.01	7.0E-02	AB018301.1	NT	TR:O50302 O60302 KIAA0555 PROTEIN . contains element MFR22 repetitive element;
234	7886	10567	1.01	7.0E-02	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
588	5761	6413	1	7.0E-02	AF007822.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
1284	6413	11589	2.66	7.0E-02	4502384	NT	Homo sapiens cytoplasmic Sepsinase truncated isoform mRNA, complete cds
2169	7282	12528	10.41	7.0E-02	5031570	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
2169	7282	12529	10.41	7.0E-02	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2533	7638	12884	1.27	7.0E-02	AF167706.1	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2687	7784	13032	10.39	7.0E-02	6005738	NT	Homo sapiens cysine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2718	7811	13066	1.19	7.0E-02	AB031007.1	NT	Homo sapiens NRAS-related gene (D1S158E), mRNA
3327	10306	13635	0.76	7.0E-02	4507500	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
3327	10308	13638	0.76	7.0E-02	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4561	8878	14818	1.17	7.0E-02	S71824.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4561	8879	14819	1.17	7.0E-02	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2880
1800	8728	13077	1.37	6.0E-02	BE390882.1	EST_HUMAN	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2880
2727	7822	13077	3.88	3.0E-02	BE589714.1	EST_HUMAN	601283012F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3805018 5'
24	5235	10349	1.34	2.0E-02	4501898	NT	601501242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3802839 5'
174	5368	10508	3.34	2.0E-02	11422948	NT	Homo sapiens activin A receptor, type IIB (ACVR2B) mRNA
174	5368	10509	3.34	2.0E-02	11422948	NT	Homo sapiens hypodermal protein dJ482023.2 (D482023.2), mRNA
748	5904	11060	4.61	2.0E-02	BE289180.1	EST_HUMAN	Homo sapiens hypodermal protein dJ482023.2 (D482023.2), mRNA
748	5904	11060	4.61	2.0E-02	BE289180.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
748	5904	11060	4.61	2.0E-02	BE289180.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'

PCT/US01/00662

Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1729	6888		1.9	2.0E-02	S78683.1	NT	mtg-mab-related [human, Genomic, 2416 nt]
1940	7059	12281	2.6	2.0E-02	AI818119.1	EST_HUMAN	w427d07.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413849 3' similar to TR:Q12844 Q12844 BREAKPOINT CLUSTER REGION PROTEIN:
1940	7059	12282	2.6	2.0E-02	AI818119.1	EST_HUMAN	w427d07.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413849 3' similar to TR:Q12844 Q12844 BREAKPOINT CLUSTER REGION PROTEIN:
1887	7084	12309	1.87	2.0E-02	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1887	7084	12310	1.97	2.0E-02	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
2040	7157	12397	7.53	2.0E-02	4508860	NT	Homo sapiens syndecan 4 (amphiglycan, syndecan) (SDC4) mRNA
2820	7719	12973	14	2.0E-02	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2760	6798	11992	1.09	2.0E-02	11418424	NT	Homo sapiens collagen, type XI, alpha 1 (COL12A1), mRNA
2760	6798	11993	1.09	2.0E-02	11418424	NT	Homo sapiens collagen, type XI, alpha 1 (COL12A1), mRNA
3597	8736	13888	1.18	2.0E-02	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3597	8736	13889	1.18	2.0E-02	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3693	8802	13958	5.99	2.0E-02	5803180	NT	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA
4263	8388	14526	1.72	2.0E-02	M10876.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
4978	10087		2.28	2.0E-02	AL040437.1	EST_HUMAN	DKFp434C0414_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFp434C0414 5'
1881	6881	12204	1.77	1.0E-02	R78078.1	EST_HUMAN	y60608.r1 Soares placenta N22-HP Homo sapiens cDNA clone IMAGE:145574 5'
1881	6881	12205	1.77	1.0E-02	R78078.1	EST_HUMAN	y60608.r1 Soares placenta N22-HP Homo sapiens cDNA clone IMAGE:145574 5'
2065	7181	12421	63.38	1.0E-02	4506688	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1), mRNA
2022	7159	12378	2.17	9.0E-03	AU121681.1	EST_HUMAN	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
2038	7154		28.89	9.0E-03	AA318723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) Homo sapiens cDNA 5' end similar to ribosomal protein L29
4312	9434	14569	1.42	9.0E-03	AU121681.1	EST_HUMAN	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
243	6434	10573	8.58	7.0E-03	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3047	8201	13367	0.87	6.0E-03	11628179	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
1391	6519	11699	4.35	6.0E-03	AB014611.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
1415	6542	11720	13.62	6.0E-03	AI674184.1	EST_HUMAN	wc08c08.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2314870 3'
1415	6542	11721	13.62	6.0E-03	AI674184.1	EST_HUMAN	wc08c08.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2314870 3'
1835	7927	12180	1.01	5.0E-03	AL291710.1	NT	Homo sapiens mRNA for CDC2L5 protein kinase, (CDC2L5 gene), isoform 2
3218	8369	13532	4.95	6.0E-03	X04201.1	NT	Human skeletal muscle 1.3 kb mRNA for tropomyosin
83	5282		4.53	4.0E-03	AA459933.1	EST_HUMAN	z650e09.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:785888 3' similar to SW:CLPA_RAT
444	5612	10757	1.44	4.0E-03	4557879	NT	P37397 CALPONIN, ACIDIC ISOFORM; Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
444	5612	10768	1.44	4.0E-03	4557879	NT	Homo sapiens Interferon gamma receptor 1 (IFNGR1) mRNA
772	5928	11084	2.86	4.0E-03	7857454	NT	Homo sapiens pascadillo (pazdriak) homolog 1, containing BRCT domain (PES1), mRNA
772	5928	11085	2.86	4.0E-03	7857454	NT	Homo sapiens pascadillo (pazdriak) homolog 1, containing BRCT domain (PES1), mRNA
1186	6319	11487	1.84	4.0E-03	8923658	NT	Homo sapiens hypothetical protein FLJ20731 (FLJ20731), mRNA
1979	7069	12327	2.52	4.0E-03	AF047677.1	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5
2225	7337	12591	1.18	4.0E-03	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
2376	7481	12735	1.31	4.0E-03	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21G101
3553	8694	13856	0.85	4.0E-03	7705398	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
4022	9154	14288	1.47	4.0E-03	4504854	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
5008	8394	13856	0.85	4.0E-03	7705398	NT	Homo sapiens tumor antigen SLP-8p (HCC8), mRNA
3629	8768	13923	0.7	3.0E-03	BF690830.1	EST_HUMAN	602246554F1 NIH MGC 62 Homo sapiens cDNA clone IMAGE:4332038 5'
3629	8768	13924	0.7	3.0E-03	BF690830.1	EST_HUMAN	602246554F1 NIH MGC 62 Homo sapiens cDNA clone IMAGE:4332038 5'
5052	10154		0.84	3.0E-03	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
187	5382	10523	26.53	2.0E-03	AB016610.1	NT	Chlorococcus eadrops mRNA for ribosomal protein S4X, complete cds
187	5382	10524	26.53	2.0E-03	AB016610.1	NT	Chlorococcus eadrops mRNA for ribosomal protein S4X, complete cds
321	5507	10646	13.27	2.0E-03	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
322	5507	10646	6.79	2.0E-03	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
2121	7236	12479	2.73	2.0E-03	U40703.1	NT	Human Cdk-associated RS cyclophilin CARS-Cyo mRNA, complete cds
2461	7655	12818	1.71	2.0E-03	BE252682.1	EST_HUMAN	60117596F1 NIH MGC 16 Homo sapiens cDNA clone IMAGE:3858220 5'
89	5308	10447	2.56	1.0E-03	AF236897.1	NT	Homo sapiens CTR1 pseudogene
89	5308	10448	2.56	1.0E-03	AF236897.1	NT	Homo sapiens CTR1 pseudogene
516	5882	10816	18.68	1.0E-03	7657016	NT	Homo sapiens hypothetical protein (D328E19.C1), mRNA
516	5882	10816	18.68	1.0E-03	7657016	NT	Homo sapiens hypothetical protein (D328E19.C1), mRNA
698	5760	10888	3.83	1.0E-03	AI146755.1	EST_HUMAN	954508.X1 NCJ CGAP CLL1 Homo sapiens cDNA clone IMAGE:1672503 3' similar to TR:Q82384 Q82384
879	6024	11195	7.53	1.0E-03	D87675.1	NT	ZINC FINGER PROTEIN ;
1240	6370	11543	9.84	1.0E-03	8923270	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1240	6370	11544	9.84	1.0E-03	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1350	6478	11658	1.17	1.0E-03	AB044783.1	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1352	6481	11660	1.18	1.0E-03	AF167106.1	NT	Homo sapiens mRNA for KIAA1563 protein, partial cds
							Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2319	7427	12679	5.52	1.0E-03	AF231881.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
2440	7544	12798	1.52	1.0E-03	AF050063.1	NT	Homo sapiens MHC class 1 region
2477	7582		1.11	1.0E-03	AL137200.1	NT	Novel human gene mapping to chromosome 1

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2782	8429	11602	2.89	1.0E-03	BE297369.1	EST_HUMAN	601177886F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532665 5'
2782	8429	11603	2.89	1.0E-03	BE297369.1	EST_HUMAN	601177886F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532665 5'
2899	8053	13222	3.67	1.0E-03	DB7675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
3201	8362		1.69	1.0E-03	AF231081.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
4407	9527	14897	1.86	1.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3935	9071	14227	1.85	6.0E-04	AF142482.1	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
1954	6976		21.18	4.0E-04	LD5094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
2618	7717	12971	1.78	4.0E-04	4808008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3649	8789	13942	1.02	4.0E-04	AW197851.1	EST_HUMAN	x89f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
3649	8789	13943	1.02	4.0E-04	AW197851.1	EST_HUMAN	x89f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
4685	9801	14947	2.87	4.0E-04	AI591312.1	EST_HUMAN	hw1110.x1 NCI_CGAP_Bn52 Homo sapiens cDNA clone IMAGE:2259403 3' similar to TR:Q18265 Q18266
608	5769	10897	3.14	3.0E-04	AB022763.1	NT	PROTEIN TYROSINE PHOSPHATASE
719	6876	11023	1.3	3.0E-04	4502506	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
1761	6877	12082	1.29	3.0E-04	AF167708.1	NT	Homo sapiens complement component 5 (C5) mRNA
1761	6877	12083	1.29	3.0E-04	AF167708.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1782	6908	12116	2.04	3.0E-04	4557558	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
4180	9289	14421	0.7	3.0E-04	AA494806.1	EST_HUMAN	Homo sapiens E1A binding protein p300 (EP300) mRNA
1441	5341	10485	3.43	1.0E-04	BE295714.1	EST_HUMAN	zw63g08.r1 Soares_Total_fetus_Nb2HF8_Ew Homo sapiens cDNA clone IMAGE:774782 5'
3061	8214	13387	2.13	1.0E-04	BE263433.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3061	8214	13388	2.13	1.0E-04	BE263433.1	EST_HUMAN	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352558 5'
4338	8468	14596	0.89	1.0E-04	9506892	NT	601111696F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352558 5'
4757	9870	15020	4.78	1.0E-04	AI804151.1	EST_HUMAN	Homo sapiens hypophyseal protein (FLJ20746), mRNA
1487	8814	11802	2.81	9.0E-05	AF027302.1	NT	CMA-BT043-080289-075 BT043 Homo sapiens cDNA
3134	8285	13441	1.02	8.0E-05	7682027	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3134	8285	13442	1.02	9.0E-05	7682027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
4509	8628	14771	1.81	8.0E-05	AI700998.1	EST_HUMAN	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
4509	8628	14772	1.81	8.0E-05	AI700998.1	EST_HUMAN	we08604.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gb:K00558
273	5463	10504	12.32	7.0E-05	DB7675.1	NT	TUBULIN ALPHA-1 CHAIN (HUMAN)
273	5463	10505	12.32	7.0E-05	DB7675.1	NT	TUBULIN ALPHA-1 CHAIN (HUMAN)
4345	9467	14605	4.62	7.0E-05	MB9708.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
						NT	Homo sapiens DNA for amyloid precursor protein, complete cds
						NT	Homo sapiens Ly-6-like protein (CD68) mRNA, complete cds

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Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4391	6611		1.35	7.0E-05	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1698	6784	11977	4.12	2.0E-05	7682027	NT	Homo sapiens KIAA0265 gene product (KIAA0265), mRNA
1698	6784	11978	4.12	2.0E-05	7682027	NT	Homo sapiens KIAA0265 gene product (KIAA0265), mRNA
1946	7083	12287	1.73	2.0E-05	4507612	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sarabry fundus dystrophy, pseudoinflammatory) (TIMP3), mRNA
1948	7098	12281	2.78	2.0E-05	BE93873.1	EST_HUMAN	801312161F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:368882 5'
2403	7609	12758	1.47	2.0E-05	5453865	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2403	7609	12759	1.47	2.0E-05	5453865	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2442	7948	12789	1.77	2.0E-05	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2484	7638	12837	2.67	2.0E-05	4758423	NT	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA
3196	8287	13444	2.69	2.0E-05	AF016462.1	NT	Homo sapiens Usurpiti-gamma mRNA, complete cds
3550	8691	13852	2.81	2.0E-05	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3550	8691	13853	2.81	2.0E-05	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3600	8739	13892	2.18	2.0E-05	AB037807.1	NT	Homo sapiens mRNA for KIAA1388 protein, partial cds
3731	8869	14022	3.84	2.0E-05	AI260264.1	EST_HUMAN	qnd1602.x1 Scores_NHMPPI_ST Homo sapiens cDNA clone IMAGE:1880546 3' similar to WP.T23G7.4
4339	9481	14598	1.62	2.0E-05	7657185	NT	CE03705 ;
5021	10123	15255	2.79	2.0E-05	7681979	NT	Homo sapiens hypothetical protein (HS222B1A), mRNA
441	7800	10754	1.39	8.0E-06	BE807607.1	EST_HUMAN	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
441	7800	10755	1.39	8.0E-06	BE807607.1	EST_HUMAN	801497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3889761 5'
5896	8022	14178	1.23	7.0E-06	AF231620.1	NT	801497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3889761 5'
2240	7351	12608	3.03	6.0E-06	BE171984.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
3299	8446	13608	0.92	6.0E-06	AL163201.2	NT	MRO-H10558-250200-002-407 HT0559 Homo sapiens cDNA
3484	8608	13770	38.6	6.0E-06	M26873.1	NT	Homo sapiens chromosome 21 segment HS21C001
6190	10287	15423	1.28	6.0E-06	AI423283.1	EST_HUMAN	Human glyceraldehyde-3-phosphate dehydrogenase pseudogene 3 end
318	6804	10842	2.15	5.0E-06	AB032898.1	NT	tf41d03.x1 NCL CGAP_Birt23 Homo sapiens cDNA clone IMAGE:2088767 3'
843	6894	11163	3.36	6.0E-06	AB032898.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
843	6894	11164	3.36	6.0E-06	AB032898.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
2583	7894		2.81	5.0E-06	11416797	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
4877	6988		1.63	5.0E-06	X60812.1	NT	H. sapiens DNA for monoclonal oxidase type A (7) (partial)
6160	10250	15389	0.86	5.0E-06	AF264760.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
4162	9288		8.24	3.0E-06	H68656.1	EST_HUMAN	y87m12H1 Scores fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:212327 5'
414	5582		3.71	2.0E-06	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (mednorne-associated) (CSPG4), mRNA

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
746	5902	11068	1.52	2.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1804	6928	12142	1.43	2.0E-08	7706205	NT	Homo sapiens CGI-201 protein (LOC61340), mRNA
4723	6937	14981	1.06	2.0E-08	BE148074.1	EST_HUMAN	RC3-H10230-040500-110-g02 HT0230 Homo sapiens cDNA
620	5780	10909	2.02	1.0E-08	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
620	5780	10910	2.02	1.0E-08	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
670	5829	10969	5.98	1.0E-08	Y18930.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1791	6917	12124	6.41	1.0E-08	AW055054.1	EST_HUMAN	EST1387124 MAGE resequences, MAGE Homo sapiens cDNA
1791	6917	12125	6.41	1.0E-08	AW055054.1	EST_HUMAN	EST1387124 MAGE resequences, MAGE Homo sapiens cDNA
2246	7878	12614	1.72	1.0E-08	U51472.2	NT	Felis catus superfast myosin heavy chain (sMYHC) mRNA, complete cds
3308	8455	13817	0.98	6.0E-07	BF245240.1	EST_HUMAN	601863712F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4081202 5'
609	6087	11255	3.71	4.0E-07	BE004436.1	EST_HUMAN	CMO-BN0108-170300-293-006 BN0108 Homo sapiens cDNA
949	6097	11265	1.34	4.0E-07	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
949	6097	11266	1.34	4.0E-07	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
1814	7033	12263	4.65	4.0E-07	5453572	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
240	5432	10571	2.11	3.0E-07	AB032868.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
876	6028	11187	14.13	3.0E-07	4502188	NT	Homo sapiens amyloid beta (A4) precursor protein (protease resistant) (APP), mRNA
876	6028	11188	14.13	3.0E-07	4502188	NT	Homo sapiens amyloid beta (A4) precursor protein (protease resistant) (APP), mRNA
1452	7018	11788	1.45	3.0E-07	4758813	NT	Homo sapiens N-myc (and STAT) Interactor (NMI), mRNA
2416	7877	12772	2.12	3.0E-07	U36265.1	NT	Human beta-prime-adaptin (BAN22) gene, exon 7
3243	8393	13555	0.89	3.0E-07	5174478	NT	Homo sapiens pericentriolar (PCNT) mRNA
4747	6850	15009	28	1.0E-07	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
902	6052	11222	6.13	9.0E-08	BE009073.1	EST_HUMAN	PM4-BT0724-010400-008-412 BT0724 Homo sapiens cDNA
1280	6409	11594	1.08	9.0E-08	8393082	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
4845	6793		1.28	9.0E-08	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1381	6509	11890	1.06	8.0E-08	AB033788.1	NT	Homo sapiens hPAD-colony10 mRNA for peptidylarginine deiminase type I, complete cds
1675	6703	11892	1.32	8.0E-08	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1675	6703	11893	1.32	8.0E-08	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1739	6968	12070	5.86	8.0E-08	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
1739	6968	12071	5.86	8.0E-08	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
3773	8910	14063	6.26	8.0E-08	J04469.1	NT	Human mitochondrial creatine kinase (CKMT) gene, complete cds
2168	7271	12519	1.29	3.0E-08	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone l8
2572	7672	12927	2.89	3.0E-08	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2712	7807		3.52	3.0E-08	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
734	5890	11042	1.37	2.0E-08	BE281694.1	EST_HUMAN	601149486F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502245 5'
2071	7187	12428	2.46	2.0E-08	BE284281.1	EST_HUMAN	601172858F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3628134 5'
2216	7331	12584	3.31	2.0E-08	AL183202.2	NT	Homo sapiens chromosome 21 segment HS21C002
3109	8282	13416	1	2.0E-08	AB032377.1	NT	Homo sapiens hCHK1 gene for checkpoint kinase, exon 2
3109	8282	13417	1	2.0E-08	AB032377.1	NT	Homo sapiens hCHK1 gene for checkpoint kinase, exon 2
4081	8210	14347	1.2	2.0E-08	8823308	NT	Homo sapiens hypothetical protein FLJ20333 (FLJ20333), mRNA
4272	8396	14535	0.69	2.0E-08	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4317	8439	14872	3.11	2.0E-08	4758331	NT	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA
4795	8908	15047	1.63	2.0E-08	AF218802.1	NT	Homo sapiens attractin precursor (ATTRN) gene, exon 18
4795	8908	15048	1.63	2.0E-08	AF218802.1	NT	Homo sapiens attractin precursor (ATTRN) gene, exon 18
5122	10223	15357	0.96	2.0E-08	AI200857.1	EST_HUMAN	q62f09.x1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1764633 3' similar to SW:CYT_COTJA
5122	10223	15357	0.96	2.0E-08	AI200857.1	EST_HUMAN	P81061 CYSTATIN ;
5122	10223	15358	0.96	2.0E-08	AI200857.1	EST_HUMAN	q62f09.x1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1764633 3' similar to SW:CYT_COTJA
405	5572	10720	80.3	1.0E-08	AI882007.1	EST_HUMAN	hw36b04.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2261743 3' similar to SW:RL28_HUMAN
454	5922	10765	3.16	1.0E-08	AW698611.1	EST_HUMAN	P23818 60S RIBOSOMAL PROTEIN L23A ;
1809	6932	12147	55.14	1.0E-08	N49818.1	EST_HUMAN	PMO-BN00655-100300-0071-408 BN00655 Homo sapiens cDNA
471	6838	10780	0.84	6.0E-09	U10991.1	NT	y23f03.1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:243565 5' similar to
3865	8001	14169	1.57	6.0E-09	AW976364.1	EST_HUMAN	PIR-S54204 S54204 ribosomal protein L28 - human ;
4713	8828	14972	1.06	6.0E-09	4502860	NT	Human G2 protein mRNA, partial cds
920	6059	11234	0.63	6.0E-09	U35484.1	NT	EST388473 IMAGE resequences, MAGN Homo sapiens cDNA
920	6059	11235	0.63	6.0E-09	U35484.1	NT	Homo sapiens CD34 antigen (CD34) mRNA
1868	7085	12311	1.27	5.0E-09	Y11365.1	NT	Human protein C inhibitor (PCHB) mRNA, complete cds
4537	8655	14800	2.03	5.0E-09	AF009660.1	NT	Human protein C inhibitor (PCHB) mRNA, complete cds
4694	8810	14957	1.06	5.0E-09	AF265555.1	NT	Human protein C inhibitor (PCHB) mRNA, complete cds
4694	8810	14958	1.06	5.0E-09	AF265555.1	NT	Human protein C inhibitor (PCHB) mRNA, complete cds
1243	8374		26.56	2.0E-09	AW274792.1	EST_HUMAN	Human Ku (p70/p80) subunit mRNA, complete cds
3242	8382	13554	1.48	2.0E-09	M30638.1	NT	Homo sapiens T cell receptor beta locus, TORB7S3A2 to TORB7S2 region
4516	9834	14779	1.05	2.0E-09	AF085703.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
							Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
							XP00906.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2738974 3' similar to gb:A31212 MYOSIN
							LIGHT CHAIN ALKALI, NON-MUSCLE ISOFORM (HUMAN);
							Human Ku (p70/p80) subunit mRNA, complete cds
							Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
313	5499	10639	1.14	1.0E-69	AF114487.1	NT	Homo sapiens intercedin long isoform (ITSN) mRNA, complete cds
377	6555	10689	1.28	1.0E-69	11628150	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
1430	6567	11740	6.38	1.0E-69	M30638.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1571	6599	11888	2.04	1.0E-69	AF192523.1	NT	Homo sapiens truncated Nucleo-Pick C3 protein (NPC3) mRNA, complete cds
1571	6599	11887	2.04	1.0E-69	AF192523.1	NT	Homo sapiens truncated Nucleo-Pick C3 protein (NPC3) mRNA, complete cds
1932	7051	12272	1.04	1.0E-69	4503730	NT	Homo sapiens FKBP6-binding protein 6 (38kD) (FKBP6) mRNA, and translated products
1932	7051	12273	1.04	1.0E-69	4503730	NT	Homo sapiens FKBP6-binding protein 6 (38kD) (FKBP6) mRNA, and translated products
3057	8210	13984	0.94	1.0E-69	J03171.1	NT	Human Interferon-alpha receptor (HuIFN-alpha-R) mRNA, complete cds
4359	9481	14619	2.23	1.0E-69	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4359	9481	14620	2.23	1.0E-69	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
1	5214	10326	1.7	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2	5214	10326	2.2	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
87	5277	10411	1.08	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
67	5277	10412	1.08	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
164	5360	10500	0.89	1.0E-100	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C048
315	5501	10941	1.29	1.0E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
341	5524	10660	2.31	1.0E-100	T05087.1	EST_HUMAN	EST T02975 Fetal brain, Strabagene (cat#93206) Homo sapiens cDNA clone HFBOR32
498	5605		1.62	1.0E-100	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
499	5657		10.45	1.0E-100	X69631.1	NT	G. gallus DNA for ZNF80 gene homolog
509	5675	10809	1.98	1.0E-100	BE180809.1	EST_HUMAN	RC3-H10675-040500-022-509 HT0625 Homo sapiens cDNA
1020	6161	11326	2.55	1.0E-100	7631686	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1020	6161	11327	2.55	1.0E-100	7631683	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1448	6674	11760	1.25	1.0E-100	BF630735.1	EST_HUMAN	502072084F1 NC1 CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215039 5'
1591	6690		1.33	1.0E-100	AW207655.1	EST_HUMAN	UHH-B1-alk-c-07-0-UI.s1 NC1 CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722184 3'
1591	6690		1.33	1.0E-100	AW207655.1	EST_HUMAN	q162109.x1 Scores Testis_NHT Homo sapiens cDNA clone IMAGE:1764633 3' similar to SW:CYT_COTJA
1596	6894	11981	1.14	1.0E-100	AI200857.1	EST_HUMAN	P81081 CYSTATIN1
1875	6995	12220	1.36	1.0E-100	A5032894.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2415	7821	12771	1.03	1.0E-100	X62468.1	NT	H. sapiens mRNA for IFN-gamma (pKc-0)
2668	7764	13015	1.78	1.0E-100	11418976	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
2690	8145		3.49	1.0E-100	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
4183	8309	14448	1.93	1.0E-100	AF057354.1	NT	Homo sapiens myofibrillar-related protein 1a mRNA, partial cds
4214	9359	14471	2.03	1.0E-100	4503792	NT	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
5079	10177	15311	3.28	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6076	10177	15312	3.28	1.0E-100	6032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
76	5285	10424	1.2	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
76	5285	10425	1.2	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
684	5842	10881	2.68	1.0E-101	AB007915.2	NT	Homo sapiens mRNA for KIAA0446 protein, partial cds
702	5859	11007	6.56	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
702	5859	11008	6.56	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
771	5825	11083	3.3	1.0E-101	7657454	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
854	6005	11178	1.87	1.0E-101	4503914	NT	Homo sapiens phosphoribosylglycine formyltransferase, phosphoribosylglycine synthetase, phosphoribosylamidimidazole synthetase (GART) mRNA
926	6074	11242	0.74	1.0E-101	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
988	6132	11303	17.11	1.0E-101	BF681218.1	EST_HUMAN	602166474F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4287281 5'
1034	6195	11359	2.32	1.0E-101	A0221878.1	EST_HUMAN	qg90909.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843338 3'
1558	6723	11817	1.18	1.0E-101	5821480	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1598	6725	11918	1.18	1.0E-101	5821480	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1758	6884	12091	1.22	1.0E-101	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1759	6884	12092	1.22	1.0E-101	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1949	7057	12282	1.42	1.0E-101	4502898	NT	Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1) mRNA
2048	7164	12403	3.43	1.0E-101	BE849070.1	EST_HUMAN	RC3-ST0281-160500-018-H09 ST0281 Homo sapiens cDNA
2329	7638	12889	1.77	1.0E-101	5729882	NT	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA
2579	7680	12835	5.26	1.0E-101	X72893.1	NT	H. sapiens EWS gene, exon 6
2708	7801	13083	3	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
2708	7801	13054	3	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
2822	8076	13500	12.48	1.0E-101	AJ252312.1	NT	Homo sapiens genomic downstream Rhesus box
3168	8337	13500	2.75	1.0E-101	4886270	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA
3225	8376	13674	2.38	1.0E-101	BF086327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882088 5'
3362	8607	13874	1.88	1.0E-101	AW065598.1	EST_HUMAN	EST377629 MAGE resequences, MAGI Homo sapiens cDNA
3381	7801	13054	1.65	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIR gene (partial), exon 12
3483	8822	13978	0.74	1.0E-101	AF073289.1	NT	Homo sapiens Na+/H+ exchanger isoform 2 (NHE2) mRNA, complete cds
3554	8880	14148	4.59	1.0E-101	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
5017	10119	15263	1.61	1.0E-101	5821480	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5017	10119	15263	1.61	1.0E-101	5821480	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
38	5248	10367	1.39	1.0E-102	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
339	5522	10657	5.21	1.0E-102	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
617	5777	10908	1.27	1.0E-102	BE262470.1	EST_HUMAN	801108292F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3344326 5'
775	5829	11088	0.98	1.0E-102	4657534	NT	Homo sapiens down-regulated in adenoma (DRA) mRNA
1118	6268	11420	5.02	1.0E-102	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1272	8401	11674	1.69	1.0E-102	11437148	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1272	8401	11675	1.69	1.0E-102	11437148	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1427	6954	11738	490.48	1.0E-102	BE408447.1	EST_HUMAN	801280882F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3626901 5'
2288	7336	12848	4.12	1.0E-102	A1124688.1	EST_HUMAN	arr60a10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1639854 3' similar to
2288	7336	12848	4.12	1.0E-102	A1124688.1	EST_HUMAN	SW:GG95_HUMAN Q08379 GOLGIN-95.;
2288	7336	12848	4.12	1.0E-102	A1124688.1	EST_HUMAN	arr60a10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1639854 3' similar to
2822	7078	13137	0.7	1.0E-102	11419442	NT	SW:GG95_HUMAN Q08379 GOLGIN-95.;
2887	6152		0.78	1.0E-102	Y13932.1	NT	Homo sapiens peroxisome biogenesis factor 1 (PEX1), mRNA
3037	6191	13347	1.83	1.0E-102	7691978	NT	Homo sapiens PRKY exon 7
3111	8264	13418	5.97	1.0E-102	AU141005.1	EST_HUMAN	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
3111	8264	13419	5.67	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
4210	6335	14467	1.54	1.0E-102	AL163207.2	NT	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
4389	8509	14651	1.93	1.0E-102	BE261310.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C007
5097	10197	15339	1.04	1.0E-103	R69488.1	EST_HUMAN	801107843F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343982 5'
68	6278	10413	2.08	1.0E-103	BE508158.1	EST_HUMAN	y32a04.r1 Soares placenta NBZHP Homo sapiens cDNA clone IMAGE:140824 5'
68	6278	10414	2.08	1.0E-103	BE508158.1	EST_HUMAN	801600405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3802305 5'
96	6306	10444	8.79	1.0E-103	D87078.2	EST_HUMAN	801300405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3802305 5'
205	5400	-10542	3.51	1.0E-103	6463793	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
862	6128	11298	0.84	1.0E-103	AJ278348.1	NT	Homo sapiens nucleolar protein (KKEID repeat) (NOP56) mRNA
1247	6377	11556	6.89	1.0E-103	BE877641.1	EST_HUMAN	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)
1609	6737	11931	3.28	1.0E-103	AF012872.1	NT	801483388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887878 5'
1817	7036	12266	1.53	1.0E-103	7697592	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
1977	7094	12323	0.99	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
1977	7094	12324	0.99	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2281	7391	12642	4.9	1.0E-103	AU194891.1	EST_HUMAN	AU194891 PLACE1 Homo sapiens cDNA clone PLACE1000665 5'
2427	7531	12784	1.1	1.0E-103	AF660563.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
2584	7685	12839	1.87	1.0E-103	N32770.1	EST_HUMAN	w691d08.s1 Soares placenta 860weeks 2NHP80cW Homo sapiens cDNA clone IMAGE:268698 3'
3041	8195		2.84	1.0E-103	BE744722.1	EST_HUMAN	601573119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834315 5'
3361	8506	13673	3.62	1.0E-103	AW298246.1	EST_HUMAN	U1H-BW0-qlh-11-0-U1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733165 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3421	8583	13720	0.97	1.0E-103	AB040882.1	NT	Homo sapiens mRNA for KIAA1458 protein, partial cds
3735	8878		14.84	1.0E-103	AF023881.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
3771	8808	14061	1.88	1.0E-103	AA485638.1	EST_HUMAN	ab10412.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element ;
3808	8846	14094	1.88	1.0E-103	11430876	NT	Homo sapiens neurotrophin 1 (NRP1), mRNA
3978	9112	14260	2.69	1.0E-103	T23683.1	EST_HUMAN	seq340 b4HB3MA-Cat108+10-B10 Homo sapiens cDNA clone b4HB3MA-Cat108+10-B10-7 3'
232	5428	10564	4.98	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072.J1 564 (synonym: hfr2) Homo sapiens cDNA clone DKFZp564H1072 6'
232	5428	10565	4.98	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072.J1 564 (synonym: hfr2) Homo sapiens cDNA clone DKFZp564H1072 6'
1898	7015	12235	1.59	1.0E-104	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteoogenic protein 8) (BMP8), mRNA
2177	7290	12537	7.35	1.0E-104	AA132976.1	EST_HUMAN	z022c08.s1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:3826438 6'
2187	7299	12548	5.57	1.0E-104	BE744828.1	EST_HUMAN	gb:Z14118 .mat CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
2349	7456	12710	1.14	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110800-214-412 CT0249 Homo sapiens cDNA
2349	7456	12711	1.14	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110800-214-412 CT0249 Homo sapiens cDNA
2414	7520	12770	7.5	1.0E-104	5031670	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2473	7577	12828	2.1	1.0E-104	7682126	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2473	7577	12829	2.1	1.0E-104	7682126	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2836	7890	13150	7.41	1.0E-104	M34871.1	NT	Human lymphocyte antigen CD59/MEK43 mRNA, complete cds
3249	8396	13568	2.55	1.0E-104	Y11151.1	NT	H. sapiens gene encoding phenylpyruvate tautomerase II
3372	8517	13568	1.02	1.0E-104	AU133928.1	EST_HUMAN	AU133928 OVARC1 Homo sapiens cDNA clone OVARC1000838 5'
3914	9060	14209	2.01	1.0E-104	AA310436.1	EST_HUMAN	EST121658 Adrenal gland tumor Homo sapiens cDNA 5' end
4101	9230	14367	1.03	1.0E-104	AB032898.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
4355	9478	14818	0.77	1.0E-104	F11748.1	EST_HUMAN	HSC31A071 normalized infant brain cDNA Homo sapiens cDNA clone c-31a07
4581	9699	14838	3.84	1.0E-104	X02761.1	NT	Human mRNA for fibronectin (FN precursor)
4581	9699	14837	2.18	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
4581	9699	14837	2.18	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
276	7881	10608	4.52	1.0E-105	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (probable neuro-in., Alzheimer disease) (APP), mRNA
424	6211	10323	39.88	1.0E-105	4505150	NT	Homo sapiens Meis1 (mouse) homolog (MEIS1) mRNA
592	5764	10881	3.78	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
592	5754	10882	3.78	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
1893	6822	12177	2.63	1.0E-105	AB020981.1	NT	Homo sapiens mRNA for cyclin B2, complete cds
1832	6855	12177	0.99	1.0E-105	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1931	7050	12271	1.54	1.0E-105	D50918.1	NT	Human mRNA for KIAA0128 gene, partial cds

Table 4

Single Exon Probes Expressed in BT474

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2172	7285	12533	65.09	1.0E-105	AA318389.1	EST_HUMAN	EST20609 Spleen 1 Homo sapiens cDNA 5' and similar to autoimmune antigen Ku, p70/p80 subunit
2302	7411		1.11	1.0E-105	BE891788.1	EST_HUMAN	601434481F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918511 5'
2683	7780		1.32	1.0E-105	AA584808.1	EST_HUMAN	no10d05.s1 NC1_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1100265 3'
2978	8132		2.66	1.0E-105	AJ22041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
3333	8478	13844	0.87	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BA228), mRNA
3333	8478	13846	0.87	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BA228), mRNA
4073	8203	14339	2.78	1.0E-105	AW691888.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C008
4918	10026		4.81	1.0E-105	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
5089	10188	15328	0.91	1.0E-105	AB018339.1	NT	Homo sapiens mRNA for KIAA0886 protein, complete cds
5130	10230	15366	1.44	1.0E-105	AB020673.1	NT	Homo sapiens mRNA for KIAA0886 protein, complete cds
146	5343		2.75	1.0E-106	AW603208.1	EST_HUMAN	U1HF-BNO-ak-g-07-Q-U1T1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
202	5397	10540	1.83	1.0E-106	AJ565055.1	EST_HUMAN	1q7601.x1 NC1_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2215008 3'
540	5708	10840	1.77	1.0E-106	AW958988.1	EST_HUMAN	EST377629 MAGC resequences, MAGC Homo sapiens cDNA
602	5784	10892	1.69	1.0E-106	J00146.1	NT	Human dihydrofolate reductase pseudogene (psd-hd1)
603	5784	10892	2.18	1.0E-106	J00146.1	NT	Human dihydrofolate reductase pseudogene (psd-hd1)
1538	6688	11852	1.83	1.0E-106	AF145712.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
1718	8843	12046	3.28	1.0E-106	U48724.1	NT	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
1815	6938	12184	2.48	1.0E-106	AA627448.1	EST_HUMAN	ng41c05.s1 NC1_CGAP_Oc8 Homo sapiens cDNA clone IMAGE:337862 3' similar to contains element LTR3 repetitive element
1816	6938	12155	2.48	1.0E-106	AA627448.1	EST_HUMAN	ng41c05.s1 NC1_CGAP_Oc8 Homo sapiens cDNA clone IMAGE:337862 3' similar to contains element LTR3 repetitive element
2114	7229	12471	1.68	1.0E-106	BE144288.1	EST_HUMAN	MRO-H10185-140200-008-410 HTD165 Homo sapiens cDNA
2285	7404	12658	12.07	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2475	7578	12831	1	1.0E-106	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2565	7668	12921	1.38	1.0E-106	U64675.2	NT	Homo sapiens sperm membrane protein BS-63 mRNA, complete cds
2567	7668	12923	1.3	1.0E-106	BE260201.1	EST_HUMAN	601149783F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3602461 5'
2721	7816	13072	9.55	1.0E-106	AJ276828.1	EST_HUMAN	gl76h10.x1 Scores_NH-MPU_S1 Homo sapiens cDNA clone IMAGE:1878307 3'
2785	6568	11755	2.61	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2785	6568	11755	2.61	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2785	6568	11755	2.61	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2840	7895	13153	1.81	1.0E-106	BE384298.1	EST_HUMAN	801272876F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3613818 5'
2807	8080	13230	4.78	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1328 protein, partial cds
2807	8080	13231	4.79	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1328 protein, partial cds
3160	8311	13471	3.81	1.0E-106	8922865	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA

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Single Exon Probes Expressed in BT474

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3160	8311	13472	3.81	1.0E-108	8822885	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3355	8500	13668	0.77	1.0E-108	AB008681.1	NT	Homo sapiens gene for actinin receptor type 1B, complete cds
3422	8684	13721	1.08	1.0E-108	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3422	8684	13722	1.08	1.0E-108	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
4012	8145	14286	7.75	1.0E-108	AW974650.1	EST_HUMAN	EST386876 IMAGE ressequencing, MAGN Homo sapiens cDNA
4012	8145	14288	7.75	1.0E-108	AW974650.1	EST_HUMAN	EST386876 IMAGE ressequencing, MAGN Homo sapiens cDNA
4031	8182	14304	1.28	1.0E-108	6728728	NT	Homo sapiens API5-like 1 (API5L1), mRNA
4471	8590	14730	1.29	1.0E-108	AA825528.1	EST_HUMAN	ef7287.1 Scans, NHMPu, S1 Homo sapiens cDNA clone IMAGE:1047688 5'
4574	8632	14828	1.05	1.0E-108	BE144286.1	EST_HUMAN	NR0-HT0165-140200-008-410 HT0165 Homo sapiens cDNA
233	6427		3.11	1.0E-107	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
262	6462		1.88	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
619	5719		4.12	1.0E-107	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM), mRNA
628	5789	10922	2.1	1.0E-107	AF155103.1	NT	Homo sapiens NY-FEN-25 antigen mRNA, partial cds
814	6867	11128	2	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
887	6037	11208	2.88	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
970	6117	11286	10.71	1.0E-107	AF164121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3), mRNA, complete cds
1262	6411	11587	2.27	1.0E-107	AB032283.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1683	6712	11803	3.58	1.0E-107	BF087405.1	EST_HUMAN	QV2-HT0540-120800-398-a05 HT0540 Homo sapiens cDNA
1764	6890	12098	2.27	1.0E-107	AF18275.1	NT	Homo sapiens cathepsin Z precursor (CTSZ), gene, exon 3
1853	6974	12185	2.84	1.0E-107	AB007822.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
1853	6974	12186	2.84	1.0E-107	AB007822.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2342	7449	12703	2.18	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-160100-001-403 CN0031 Homo sapiens cDNA
2342	7449	12704	2.18	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-160100-001-403 CN0031 Homo sapiens cDNA
2508	7609	12860	1.51	1.0E-107	BE732460.1	EST_HUMAN	601597619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 6'
2508	7609	12861	1.51	1.0E-107	BE732460.1	EST_HUMAN	601597619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2678	8133	13286	4.88	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-160100-001-403 CN0031 Homo sapiens cDNA
2678	8133	13286	4.88	1.0E-107	AW842451.1	EST_HUMAN	PM1-CN0031-160100-001-403 CN0031 Homo sapiens cDNA
3074	8227	13378	3.46	1.0E-107	5802097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
3806	8942	14090	4.44	1.0E-107	AF020871.1	NT	Homo sapiens myotubularin (MTM1), gene, exon 9
866	6104	11273	2.51	1.0E-108	BE288042.1	EST_HUMAN	601177018F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532348 5'
1269	6398	11671	6.07	1.0E-108	Y18900.1	NT	Homo sapiens NF2 gene
2070	7188	12427	2.92	1.0E-108	BF028728.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954839 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2311	7420	12670	1.13	1.0E-108	AI686040.1	EST_HUMAN	U01610.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2246938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
2311	7420	12671	1.13	1.0E-108	AI686040.1	EST_HUMAN	U01610.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2246938 3' similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
2405	7511	12761	65.49	1.0E-108	BE206864.1	EST_HUMAN	bb25x10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2863899 3' similar to gb:X63777 80S RIBOSOMAL PROTEIN L23 (HUMAN); db:J06277 Mouse hexokinase mRNA, complete cds (MOUSE);
2926	8083	13250	1.27	1.0E-108	6006976	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3331	8477	13840	0.63	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
3331	8477	13841	0.63	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4128	9257	14395	1.35	1.0E-108	AW664438.1	EST_HUMAN	HIT2a11.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872060 3' similar to SW/3BP1_MOUSE P65194 SH3-BINDING PROTEIN 3BP-1.;
4500	9616	14760	5.12	1.0E-108	U72661.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4500	9616	14761	5.12	1.0E-108	U72661.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4772	9885	15031	2.17	1.0E-108	7681979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4897	10008	15153	1.09	1.0E-108	AW504789.1	EST_HUMAN	U14F-BNO-ain-04-0-UI-1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080188 5'
4927	10037	15177	2.75	1.0E-108	AJ008005.1	NT	Homo sapiens PSN1 gene, alternative transcript
5116	10217	15352	0.67	1.0E-108	5031824	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
5141	10241	15377	1.15	1.0E-108	Y12490.1	NT	Homo sapiens mRNA for Golgi-associated microtubule-binding protein (GMAP-210)
5149	10249	15388	1.49	1.0E-108	8400716	NT	Homo sapiens nabulin (NEB), mRNA
5204	10301		3.35	1.0E-108	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
41	5252	10370	2.06	1.0E-109	AW603116.1	EST_HUMAN	IL2-UM0077-280-400-078-D08 UM0077 Homo sapiens cDNA
64	5274	10409	3.56	1.0E-109	D86897.1	NT	Human mRNA for KIAA0220 gene, partial cds
216	5410	10550	0.72	1.0E-109	11422488	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
225	5418	10555	4.64	1.0E-109	11438391	NT	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
498	5634	10772	4.05	1.0E-109	4507712	NT	Homo sapiens tetrapeptide repeat domain 2 (TTC2) mRNA
596	5758	10886	26.83	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
596	5758	10887	26.83	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1013	6156	11322	0.61	1.0E-109	M28689.1	NT	Homo sapiens chromosome 21 segment HS21C049
1205	6338	11508	37.97	1.0E-109	M28689.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
1205	6338	11509	20.28	1.0E-109	M28689.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
1556	6885	11872	2.97	1.0E-109	BE283673.1	EST_HUMAN	601186922F2 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2959638 5'
1556	6885	11873	2.97	1.0E-109	BE283673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959638 5'
1884	7004	12223	9.05	1.0E-109	D13643.2	NT	Homo sapiens mRNA for KIAA0018 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2223	7335	12589	1.78	1.0E-109	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2231	7343	12597	3.7	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
2587	7698	12943	4.69	1.0E-109	A022328.1	EST_HUMAN	ov65a01.x1 Soares fetal_liver spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR-O02197 O02197 CIRCULATING CATHODIC ANTIGEN.;
2587	7698	12944	4.89	1.0E-109	A022328.1	EST_HUMAN	ov65a01.x1 Soares fetal_liver spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR-O02197 O02197 CIRCULATING CATHODIC ANTIGEN.;
2588	7699	12946	1.95	1.0E-109	4504208	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
3030	8184	13339	2.43	1.0E-109	N85190.1	EST_HUMAN	J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC FINGER PROTEIN ZNF43
3369	8514	13681	1.01	1.0E-109	AW593192.1	EST_HUMAN	GM3-NN0009-180400-150-f10 NN0009 Homo sapiens cDNA
3369	8514	13692	1.01	1.0E-109	AW593192.1	EST_HUMAN	GM3-NN0009-180400-150-f10 NN0009 Homo sapiens cDNA
3503	8644	13810	1.13	1.0E-109	AF240888.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3545	8686	13848	0.89	1.0E-109	M37628.1	NT	Homo sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 8-10
3545	8688	13849	0.89	1.0E-109	M37628.1	NT	Homo sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 8-10
3819	8959		1.26	1.0E-109	BE146144.1	EST_HUMAN	MRO-HT0209-110400-108-c04 HT0209 Homo sapiens cDNA
3888	9103	14251	0.87	1.0E-109	AB011181.2	NT	Homo sapiens mRNA for KIAA0609 protein, partial cds
3968	9103	14252	0.87	1.0E-109	AB011181.2	NT	Homo sapiens mRNA for KIAA0609 protein, partial cds
4118	9248	14383	3.75	1.0E-109	AI655417.1	EST_HUMAN	ts99a06.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2293330 3' similar to WP:FS3A2.8 CE16100;
4383	9504	14647	2.77	1.0E-109	4504208	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
4573	8691	14828	1.59	1.0E-109	7682083	NT	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
4904	10014	15156	0.69	1.0E-109	R15400.1	EST_HUMAN	ys48a06.t1 Soares infant brain N1B Homo sapiens cDNA clone IMAGE:55057 5'
5034	10136	15268	0.63	1.0E-109	BE283873.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859638 5'
5034	10138	15269	0.63	1.0E-109	BE283873.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859638 5'
3	5216	10327	0.76	1.0E-110	7649804	NT	Homo sapiens deiodinase, lactoferrin, type II (DIO2), transcript variant 2, mRNA
38	5247	10384	3.66	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
38	5247	10385	3.68	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
105	5219	10327	0.86	1.0E-110	7649804	NT	Homo sapiens deiodinase, lactoferrin, type II (DIO2), transcript variant 2, mRNA
292	5480	10622	0.76	1.0E-110	D87291.1	NT	Human mRNA for inward rectifier potassium channel, complete cds
525	5691	10823	1.39	1.0E-110	U84550.1	NT	Human dystrobrevin (DTN) gene, exon 20
1182	6317	11465	1.01	1.0E-110	5031620	NT	Homo sapiens calcitonin receptor-like (CALCR) mRNA
1283	6412	11698	2.49	1.0E-110	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1926	7045	12268	1.67	1.0E-110	BE378477.1	EST_HUMAN	601237545F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609883 5'
2050	7166		0.98	1.0E-110	BF508886.1	EST_HUMAN	UHH-BI4-acc-b-05-0-UJ.61 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2803	7959		0.88	1.0E-110	4503088	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (GSPG4), mRNA
3002	6412	11888	1.48	1.0E-110	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
3059	8212		1.12	1.0E-110	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
4175	8301	14437	2.25	1.0E-110	M15918.1	NT	Human autophagosome antigen small nuclear ribonucleoprotein E pseudogene
4803	8721	14856	2.31	1.0E-110	A017218.1	EST_HUMAN	cd22610.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1827683 3' similar to SW:1121, RAT P62591 HOMO sapiens cDNA clone HEMBA1002241 5'
4823	8741	14883	4.09	1.0E-110	AU117812.1	EST_HUMAN	AU117812 HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5'
4898	10066		2.28	1.0E-110	7682441	NT	Homo sapiens KIAA1002 protein (KIAA1002), mRNA
6165	10283	15402	7.72	1.0E-110	A1791382.1	EST_HUMAN	cd4402.y5 NCI_CGAP_Kd5 Homo sapiens cDNA clone IMAGE:1471779 5'
170	6365		42.78	1.0E-111	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
193	5388	10831	0.61	1.0E-111	4758807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
733	5889		2.03	1.0E-111	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3882088 5'
742	5898	11051	3.32	1.0E-111	8393092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
928	6076	11245	2.2	1.0E-111	M25142.1	NT	Homo sapiens cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34
3877	8816	13872	1.05	1.0E-111	6912841	NT	Homo sapiens sex comb on midleg homolog 1 (SCMH1), mRNA
3877	8816	13873	1.05	1.0E-111	6912841	NT	Homo sapiens sex comb on midleg homolog 1 (SCMH1), mRNA
4142	8270	14403	1.08	1.0E-111	7681569	NT	Homo sapiens DKFZP434D158 protein (DKFZP434D158), mRNA
4306	9428	14563	4.63	1.0E-111	K02288.1	NT	Human encephalin B (enkb) gene, exon 4 and 3' flank and complete cds
605	5765	10893	0.78	1.0E-112	4601854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
607	5767	10895	4.13	1.0E-112	U28103.1	NT	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
607	5767	10896	4.13	1.0E-112	U28103.1	NT	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
631	5761	10824	1.88	1.0E-112	BF509039.1	EST_HUMAN	U1-H-B14-ex1-g-04-U1-g1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
631	5791	10825	1.88	1.0E-112	BF509039.1	EST_HUMAN	U1-H-B14-ex1-g-04-U1-g1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
1002	8148	11315	1.22	1.0E-112	AF167623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1063	8204	11368	2.27	1.0E-112	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
1698	8226	12025	4.1	1.0E-112	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1698	8226	12026	4.1	1.0E-112	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
2181	7294	12541	0.88	1.0E-112	A176826.1	EST_HUMAN	w80008.x1 NCI_CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2400811 3'
2478	7583	12833	1.67	1.0E-112	BE86859.1	EST_HUMAN	601442874F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3846868 5'
3050	8204		0.78	1.0E-112	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3861	8597	14164	0.66	1.0E-112	BE076073.1	EST_HUMAN	MR2-BT0590-090300-113-109 BT0590 Homo sapiens cDNA
4577	8695	14832	0.8	1.0E-112	4504118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4717	8832	14975	5.79	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds

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Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4717	6832	14976	5.78	1.0E-112	AB037632.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
741	5897	11049	7.68	1.0E-113	AJ365588.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1853625 3'
741	5897	11050	7.68	1.0E-113	AJ365588.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1853625 3'
942	6090	11268	39.89	1.0E-113	M11985.1	NT	Human X-linked phosphoglycerate kinase gene, exon 8
1555	6884	11871	3.48	1.0E-113	AJ365588.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1853625 3'
1943	7873	12285	1.77	1.0E-113	AF240775.1	NT	Homo sapiens eIF4E-transporter mRNA, complete cds
2088	7202	12448	1.23	1.0E-113	BF515218.1	EST_HUMAN	U14-BW1-anL403-Q-U1.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082878 3'
2431	7535	12768	4.66	1.0E-113	AJ005976.1	NT	Homo sapiens PLP gene
3107	8260	13414	3.18	1.0E-113	AJ223948.1	NT	Homo sapiens mRNA for putative RNA helicase, 3' and
5049	10161	15281	0.6	1.0E-113	5453562	NT	Homo sapiens activating transcription factor B (B-ATF), mRNA
5049	10161	15282	0.6	1.0E-113	5453562	NT	Homo sapiens activating transcription factor B (B-ATF), mRNA
57	5268	10397	3.85	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
57	5268	10398	3.85	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
57	5268	10399	3.85	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
944	5805	10840	5.72	1.0E-114	T70551.1	EST_HUMAN	y415d01.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108288 3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN)/contains Alu repetitive element;
1072	6212	11376	4.74	1.0E-114	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1317	6446	11625	7.17	1.0E-114	7657629	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1654	6782	11975	3.61	1.0E-114	8631094	NT	Homo sapiens inhibitory chromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
1689	6816	12013	10.89	1.0E-114	8678073	NT	Homo sapiens nucleocytin-like protein 1 (NLP_1), mRNA
2074	7190	12433	3.62	1.0E-114	BE171864.1	EST_HUMAN	MRO-HT0559-25020-002-d07 HT0559 Homo sapiens cDNA
2236	7348	12603	1.19	1.0E-114	AB002374.1	NT	Homo sapiens mRNA for KIAA0378 gene, partial cds
2765	5254	10373	1.13	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
2765	5254	10374	1.13	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3108	8281	13416	2.8	1.0E-114	X04089.1	NT	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3161	8302	13482	1.01	1.0E-114	BF206374.1	EST_HUMAN	601896632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5'
3991	9126	14270	1.35	1.0E-114	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4192	9318	14451	1	1.0E-114	AA574958.1	EST_HUMAN	nk11d02.s1 NCI_CGAP_Os2 Homo sapiens cDNA clone IMAGE:1013187 3' similar to gb:X65857_cds1
4369	9490	14634	0.78	1.0E-114	J03171.1	NT	OLFACTORY RECEPTOR-LIKE PROTEIN HGMPO7E (HUMAN);
5118	10219	19353	1.43	1.0E-114	BE275324.1	EST_HUMAN	Human interferon-alpha receptor (HuIFN-alpha-Rce) mRNA, complete cds
22	5233	10347	10.03	1.0E-115	4758111	NT	601122173F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346098 5'
125	5323	10468	4.96	1.0E-115	4505939	NT	Homo sapiens HLA-B associated transcript-1 (D6581E) mRNA
							Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA

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Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
129	5327		52.4	1.0E-115	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
200	5478	10819	9.75	1.0E-115	AW804769.1	EST_HUMAN	QV4-JM0094-300300-158-508 UM0094 Homo sapiens cDNA
534	5700	10832	1.52	1.0E-115	AI339208.1	EST_HUMAN	Q0601.1x1 NCL CGAP GC4 Homo sapiens cDNA clone IMAGE:1948809 3' similar to TR:O00536 O00536 TTFJ INTERACTING PEPTIDE 5;
534	5700	10833	1.52	1.0E-115	AI339206.1	EST_HUMAN	Q0601.1x1 NCL CGAP GC4 Homo sapiens cDNA clone IMAGE:1948809 3' similar to TR:O00536 O00536 TTFJ INTERACTING PEPTIDE 5;
787	6941	11100	1.28	1.0E-115	6174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
787	6941	11101	1.26	1.0E-115	6174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
789	6943	11103	198.09	1.0E-115	4603794	NT	Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA
1574	8702	11890	1.49	1.0E-115	AF228180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1574	8702	11891	1.49	1.0E-115	AF228180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1840	8361	12184	1.89	1.0E-115	AJ277832.1	NT	Homo sapiens partial TTN gene for titin
2072	7188	12425	1.22	1.0E-115	BE745469.1	EST_HUMAN	601576838F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3928832 5'
2072	7188	12430	1.22	1.0E-115	BE745469.1	EST_HUMAN	601576838F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3928832 5'
2276	7385	12634	1.35	1.0E-115	AF231124.1	NT	Homo sapiens testican-1 mRNA, complete cds
2813	7989		1.84	1.0E-115	AW804769.1	EST_HUMAN	QV4-JM0094-300300-158-508 UM0094 Homo sapiens cDNA
3091	8244	13394	3.74	1.0E-115	AJ246922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3091	8244	13395	3.74	1.0E-115	AJ246922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3454	8598	13760	2.04	1.0E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
4016	9149	14291	4.51	1.0E-115	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4240	9365	14498	0.73	1.0E-115	AL137163.1	NT	Novel human gene mapping to chromosome X
4360	9301	14644	3.37	1.0E-115	6912669	NT	Homo sapiens sir2-like 3 (SIRT3), mRNA
4413	9333	14672	3.17	1.0E-115	4788276	NT	Homo sapiens EphA4 (EPHA4) mRNA
4647	9786	14809	3.38	1.0E-115	AL088857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4647	9786	14910	3.36	1.0E-115	AL088857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4878	9890	15138	2.95	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4878	9890	15137	2.95	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
571	5735	10863	1.37	1.0E-115	BE275502.1	EST_HUMAN	601121347F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:2888875 5'
801	6585	11115	1.24	1.0E-115	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
860	6911		0.63	1.0E-115	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
1998	7115	12560	1.69	1.0E-115	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
1998	7115	12561	1.69	1.0E-115	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
2018	7136	12376	2.34	1.0E-115	AJ130380.1	EST_HUMAN	AU133080 NT2RP4 Homo sapiens cDNA clone NT2RP4001228 5'
2088	7632	12447	1.18	1.0E-115	M19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18

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Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2088	7832	12448	1.18	1.0E-116	M18824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2284	7393	12844	1.09	1.0E-116	5453841	NT	Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA
2322	7430		1.27	1.0E-116	U78308.1	NT	Human olfactory receptor pseudo_cdf17-201-1 (OR17-201-1) pseudogene, complete cds
2433	7537	12760	2.13	1.0E-116	AB018333.1	NT	olfactory receptor pseudo_cdf17-01 (OR17-01) pseudogene, complete cds
2686	7880	13043	4.58	1.0E-116	BE880256.1	EST_HUMAN	Homo sapiens mRNA for KIAA0750 protein, partial cds
3154	8305	13484	5.48	1.0E-116	L77670.1	NT	501513337F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914600 5'
3154	8305	13485	5.48	1.0E-116	L77670.1	NT	Homo sapiens Df(George) syndrome critical region, centromeric end
4357	8478	14817	2.21	1.0E-116	5031684	NT	Homo sapiens Df(George) syndrome critical region, centromeric end
4453	9572	14711	1.62	1.0E-116	AB028398.1	NT	Homo sapiens sodium phosphate transporter 3 (NPT3) mRNA
4826	9837	15078	1.68	1.0E-116	AB070686.1	EST_HUMAN	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5033	10135	15266	1.18	1.0E-116	U58109.1	NT	PM-BT135-070409-018 BT135 Homo sapiens cDNA
5033	10135	15267	1.18	1.0E-116	U58109.1	NT	Mus musculus nebulin mRNA, partial cds
557	5722	10853	9.68	1.0E-117	4826836	NT	Mus musculus nebulin mRNA, partial cds
1078	7808	11384	2.2	1.0E-117	AF124383.1	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
1228	6360	11630	1.2	1.0E-117	AF124383.1	NT	Mus musculus fragile-X-related protein 1 (Fxr1h) gene, exons 13a through 15
1846	6968	12187	1.38	1.0E-117	M16816.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2183	7305	12555	3.45	1.0E-117	AW057899.1	EST_HUMAN	Human apolipoprotein B-100 (apoB) gene, exon 10
3251	8401	13563	1.68	1.0E-117	AA978114.1	EST_HUMAN	EST1369769 IMAGE resequencing, IMAGE Homo sapiens cDNA
3985	9100	14240	5.62	1.0E-117	AA316723.1	EST_HUMAN	op32x11.57 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:1878548 3'
4321	9443	14576	1.78	1.0E-117	8858584	NT	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L28
4550	9668	14810	3.06	1.0E-117	AL042120.1	EST_HUMAN	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
4692	9808	14954	1.08	1.0E-117	X88870.1	NT	DKFZp434C1120_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434C1120 5'
4692	9808	14955	1.08	1.0E-117	X88870.1	NT	H. sapiens mRNA for TPOR18 protein
4778	9891	15037	10.28	1.0E-117	AF134304.2	NT	H. sapiens mRNA for TPOR18 protein
4778	9891	15038	10.28	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4839	9951	15095	1.5	1.0E-117	U58109.1	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4839	9951	15096	1.5	1.0E-117	U58109.1	NT	Mus musculus nebulin mRNA, partial cds
4917	10027	15169	3.3	1.0E-117	AB020673.1	NT	Mus musculus nebulin mRNA, partial cds
66	5278	10416	7.78	1.0E-118	AF161500.1	NT	Homo sapiens mRNA for KIAA0888 protein, complete cds
91	5300	10438	1.93	1.0E-118	AL045854.1	EST_HUMAN	Homo sapiens HSPC151 mRNA, complete cds
515	5681	10815	11.4	1.0E-118	7657016	NT	DKFZp434056_r1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434056 5'
							Homo sapiens hypothetical protein (D328E19.C1), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
915	7804	11231	2.6	1.0E-118	5174880	NT	Homo sapiens sine oculis homeobox (Drosophila) homolog 1 (SIX1) mRNA
2214	7326	12676	3.87	1.0E-118	BE389705.1	EST_HUMAN	601281847F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 6'
2214	7326	12677	3.87	1.0E-118	BE389705.1	EST_HUMAN	601281847F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 6'
2214	7326	12678	3.87	1.0E-118	BE389705.1	EST_HUMAN	601281847F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2310	7419		19.78	1.0E-118	AW951728.1	EST_HUMAN	EST363769 IMAGE resequencing, MAGB Homo sapiens cDNA
2703	7789	13050	8.32	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
2703	7799	13051	8.32	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
3080	8233		4.24	1.0E-118	Y13832.1	NT	Homo sapiens PRKY exon 7
3178	8328	13492	4.93	1.0E-118	A347694.1	EST_HUMAN	qp01605.X1 NCI CGAP Kids Homo sapiens cDNA clone IMAGE:1916769 3'
3178	8328	13493	4.93	1.0E-118	A347694.1	EST_HUMAN	qp01605.X1 NCI CGAP Kids Homo sapiens cDNA clone IMAGE:1916769 3'
3921	8057	14216	0.98	1.0E-118	AB024469.1	NT	Pongo pygmaeus DNA, similar to pol gene of HERV-W and MSRV, isolate:ORW3-3
4065	9195	14334	8.96	1.0E-118	D23660.1	NT	Human mRNA for ribosomal protein, complete cds
4675	6791	14937	1.17	1.0E-118	11425763	NT	Homo sapiens KIAA0478 gene product (KIAA0478), mRNA
769	6911	11069	0.63	1.0E-119	AF170492.1	NT	Homo sapiens chloride channel CLCA4 (CLCA4) mRNA, complete cds
1039	7607	11344	1.69	1.0E-119	7705807	NT	Homo sapiens CGI-105 protein (LOC51011), mRNA
1837	7056	12277	3.87	1.0E-119	AB023147.1	NT	Homo sapiens mRNA for KIAA0930 protein, partial cds
3077	8230	13382	0.94	1.0E-119	8922205	NT	Homo sapiens hypothetical protein FLJ10052 (FLJ10052), mRNA
3826	9081	14219	1.07	1.0E-119	4804118	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
266	5487	10628	0.77	1.0E-120	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
1043	6184	11360	2.38	1.0E-120	AF248540.1	NT	Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds
1043	6184	11351	2.38	1.0E-120	AF248540.1	NT	Homo sapiens Intersectin 2 (SH3D1B) mRNA, complete cds
1434	6591	11744	6.03	1.0E-120	N44873.1	EST_HUMAN	Y940g12.L1 Soares melanocyte 2/Nb1M Homo sapiens cDNA clone IMAGE:273766 5'
1616	6743	11938	2.55	1.0E-120	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S62 precursor, mRNA, complete cds
1616	6941	12159	4.32	1.0E-120	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2088	7213	12460	2.02	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2088	7213	12461	2.02	1.0E-120	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
2500	7804	12852	1.23	1.0E-120	4755124	NT	Homo sapiens aquaporin 4 (AQP4), splice variant b, mRNA
3289	5487	10628	1.13	1.0E-120	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
4336	9457	14594	1.71	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4335	9457	14595	1.71	1.0E-120	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4632	9750	14896	1.79	1.0E-120	AF098463.1	NT	Homo sapiens stannocalcin (STC) gene, partial cds
4632	9750	14897	1.79	1.0E-120	AF098463.1	NT	Homo sapiens stannocalcin (STC) gene, partial cds
72	5281	10419	0.87	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
378	5554	10698	2.09	1.0E-121	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 8'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
722	7898	11028	1.11	1.0E-121	6032182	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
1597	8718	11908	0.89	1.0E-121	AB011183.1	NT	Homo sapiens mRNA for KIAA0381 protein, partial cds
1969	7088	12312	1.31	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate 4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
1969	7088	12313	1.31	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate 4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
2083	7208	12464	1.15	1.0E-121	L76631.1	NT	Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds
2540	7943	12892	1.37	1.0E-121	BF344378.1	EST_HUMAN	602014759F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150288 5'
2540	7943	12893	1.37	1.0E-121	BF344378.1	EST_HUMAN	602014759F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150288 5'
2938	8092	13259	1.11	1.0E-121	AF11168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
3053	8208	13381	5.9	1.0E-121	Y18208.1	NT	Homo sapiens HHB3 gene for hair keratin, exons 1 to 9
3053	8208	13382	5.9	1.0E-121	Y18208.1	NT	Homo sapiens HHB3 gene for hair keratin, exons 1 to 9
3524	8065	13832	1	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3524	8065	13833	1	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3655	8794	13950	7.87	1.0E-121	AF165166.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds
3704	8842	13957	0.7	1.0E-121	AI804151.1	EST_HUMAN	CHI-BT043-090289-078 BT043 Homo sapiens cDNA
4307	9428	14864	1.48	1.0E-121	AI263294.1	EST_HUMAN	gs57601.x1 NCI_CGAP_Part1 Homo sapiens cDNA clone IMAGE:2005417 3'
4861	10086	15205	2.74	1.0E-121	X91837.1	NT	H. sapiens ECE-1 gene (exon 17)
265	5455	10593	1.76	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
334	5517	10653	2.2	1.0E-122	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
366	5636	10877	1.86	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
883	6053	11205	3.01	1.0E-122	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
1222	8354	11524	5.81	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
1727	8854	12059	2.28	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1727	8854	12060	2.28	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1828	8049	12171	3.48	1.0E-122	BE908024.1	EST_HUMAN	601497032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3888358 5'
2494	7568	12821	22.83	1.0E-122	BF316170.1	EST_HUMAN	601886173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2494	7568	12822	22.83	1.0E-122	BF316170.1	EST_HUMAN	601886173F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4125234 5'
2801	7058	13122	2.09	1.0E-122	AF284717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
4815	5827	15068	2.79	1.0E-122	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease resistant) (APP), mRNA
4975	10083		1.34	1.0E-122	AW504645.1	EST_HUMAN	U1-HF-BND-af-e-03-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078948 5'

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Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
188	5380	10521	0.84	1.0E-123	U31519.1	NT	Human phosphoenolpyruvate carboxylase (PCK1) gene, promoter region and partial cds
768	6022	11078	2.81	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
768	6822	11080	2.91	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
1014	6167	11323	4.65	1.0E-123	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C049
1023	6164	11330	5.91	1.0E-123	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1242	6372	11547	11.95	1.0E-123	4508818	NT	Homo sapiens phosphatidylinositol-4-phosphate 6-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1242	6372	11548	11.85	1.0E-123	4508818	NT	Homo sapiens phosphatidylinositol-4-phosphate 6-kinase, type II, beta (PIP5K2B) mRNA, and translated products
2080	7205	12450	2.04	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2080	7205	12451	2.04	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2080	7205	12452	2.04	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2263	7402	12452	1.8	1.0E-123	7705982	NT	Homo sapiens RAB9-like protein (LOG51209), mRNA
268	6458	10594	1.8	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
268	6458	10595	1.8	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
272	6482	10782	1.57	1.0E-124	D87876.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
485	5853	10782	2.1	1.0E-124	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
689	6848	10988	3.14	1.0E-124	AA397551.1	EST_HUMAN	Z87b04.J1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
689	6848	10989	3.14	1.0E-124	AA397551.1	EST_HUMAN	G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
757	5912	11070	6.92	1.0E-124	AF155854.1	NT	Z87b04.J1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
809	6382	11124	1.68	1.0E-124	4507500	NT	G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
905	6055	11224	3.62	1.0E-124	7709448	NT	Human putative ribosomal protein S1 mRNA
1319	6448	11628	0.74	1.0E-124	11418092	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1353	6482	11681	4.17	1.0E-124	AF274892.1	NT	Homo sapiens ring finger protein (RNF), mRNA
1353	6482	11682	4.17	1.0E-124	AF274892.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1827	6850	12172	3.71	1.0E-124	AJ131712.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
2054	7170	12409	1.39	1.0E-124	BE870824.1	EST_HUMAN	Homo sapiens mRNA for nuclear RNA-helicase (ncl-h81 gene)
2434	7538	12781	1.68	1.0E-124	AB024059.1	NT	601481715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3883954 5'
3471	6813	13779	0.84	1.0E-124	S78884.1	NT	Homo sapiens gene for B120, exon 11
3471	6813	13780	0.84	1.0E-124	S78884.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3471	6813	13780	0.84	1.0E-124	S78884.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon
3878	8012	14169	0.8	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4051	9182	14324	0.73	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA

Table 4

Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4710	9828	14969	1.71	1.0E-124	AB024089.1	NT	Homo sapiens gene for B120, exon 11
317	5503		11.1	1.0E-125	AB032898.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
426	5212	10324	3.84	1.0E-126	BE749822.1	EST_HUMAN	601577681F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3828885 5'
643	5804	10938	0.64	1.0E-125	A1110656.1	EST_HUMAN	HA0088 Human fetal liver cDNA library Homo sapiens cDNA
643	5804	10939	0.84	1.0E-126	A1110656.1	EST_HUMAN	HA0088 Human fetal liver cDNA library Homo sapiens cDNA
726	5882	11030	1.81	1.0E-125	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
881	6012	11183	3.17	1.0E-125	AA042813.1	EST_HUMAN	2453c07.s1 Soares_pregnant_uterus_NIHPU Homo sapiens cDNA clone IMAGE:468540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMPO7E (HUMAN);
889	6145	11312	1.51	1.0E-125	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1155	6251	11454	1.2	1.0E-125	7682279	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
1823	6946	12167	3.81	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
1823	6946	12168	3.81	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
2338	7445	12697	2.88	1.0E-125	AA011278.1	EST_HUMAN	2401g09.r1 Soares_fetal_liver_spleen_TNFSL_ST Homo sapiens cDNA clone IMAGE:429568 5'
2474	7578	12830	2.08	1.0E-125	AA042813.1	EST_HUMAN	2453c07.s1 Soares_pregnant_uterus_NIHPU Homo sapiens cDNA clone IMAGE:468540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMPO7E (HUMAN);
2559	7681	12814	1.68	1.0E-125	4504698	NT	Homo sapiens inhibin, alpha (INH4) mRNA
2559	7681	12815	1.68	1.0E-125	4504698	NT	Homo sapiens inhibin, alpha (INH4) mRNA
2563	7684	12819	11.32	1.0E-125	A1732666.1	EST_HUMAN	cb84d02.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1471779 3'
2681	10303	13289	1	1.0E-125	BE018009.1	EST_HUMAN	bb74f08.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048131 5' similar to TR:O85604 O85604 ZINC FINGER PROTEIN;
3837	8973	14129	1.42	1.0E-125	AA042813.1	EST_HUMAN	2453c07.s1 Soares_pregnant_uterus_NIHPU Homo sapiens cDNA clone IMAGE:468540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMPO7E (HUMAN);
4323	8641	14788	1.94	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4523	8641	14789	1.94	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4588	9706	14844	1.98	1.0E-125	BES16412.1	EST_HUMAN	60114152F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140768 5'
774	6928	11087	2.04	1.0E-126	4788007	NT	Homo sapiens CDC-like kinase (CLK) mRNA
777	6931	11090	1.04	1.0E-126	M61836.1	NT	Human laminin B1 chain gene, exon 20
919	6068	11233	0.97	1.0E-126	X68735.1	NT	H. sapiens gene for alphet-antichymotrypsin, exon 3
2325	7433	12895	1.42	1.0E-126	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
2326	7433	12896	1.42	1.0E-126	8923056	NT	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
2560	7682	12816	3.07	1.0E-126	6382078	NT	Homo sapiens RAN binding protein 2 (RANBP2), mRNA
3044	8198	13554	7.24	1.0E-126	AA160709.1	EST_HUMAN	2a72c03.r1 Striatogene pancreas (#837208) Homo sapiens cDNA clone IMAGE:582420 5'
3044	8198	13555	7.24	1.0E-126	AA160709.1	EST_HUMAN	2a72c03.r1 Striatogene pancreas (#837208) Homo sapiens cDNA clone IMAGE:582420 5'
3608	8748	13904	1.24	1.0E-126	X63941.1	NT	H. sapiens DNA for liver cytochrome b5 pseudogene

Table 4

Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3632	8771	13927	2.35	1.0E-128	7657038	NT	Homo sapiens death receptor 8 (DR8), mRNA
4802	9916	15036	1.57	1.0E-128	N34078.1	EST_HUMAN	y78c06.r1 Soares melanocyte ZNbl-HM Homo sapiens cDNA clone IMAGE:267850 5'
167	5363	10504	8.45	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
167	5363	10505	8.46	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
168	5363	10504	7	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
168	5363	10505	7	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
271	6481	10602	1.52	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
271	6481	10603	1.52	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
882	6032	11204	1.34	1.0E-127	AF114488.1	NT	Homo sapiens ubiquitin short isoform (ITSN) mRNA, complete cds
1705	6833	12034	1.59	1.0E-127	4827053	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
2058	7174	12412	1.79	1.0E-127	5803055	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2058	7174	12413	1.79	1.0E-127	5803055	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2184	7287	12549	47.43	1.0E-127	4506820	NT	Homo sapiens ribosomal protein L28 (RPL28) mRNA
2323	7431	12683	3.12	1.0E-127	AF245505.1	NT	Homo sapiens adicican mRNA, complete cds
2573	7673	12928	49.35	1.0E-127	X12881.1	NT	Human mRNA for cytochrome 18
2585	7686	12940	1	1.0E-127	AA460181.1	EST_HUMAN	z432a02.r1 Soares_tetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789098 5'
2585	7686	12941	1	1.0E-127	AA450131.1	EST_HUMAN	z432a02.r1 Soares_tetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789098 5'
3788	8925	14075	1	1.0E-127	AW161287.1	EST_HUMAN	au06a08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782594 5' similar to TR:Q16170 Q16170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ;contains element MER22 repetitive element;
4230	9355	14487	19.81	1.0E-127	7708238	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4230	9355	14488	19.81	1.0E-127	7708238	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4473	9592	14731	0.79	1.0E-127	AF252297.1	NT	Homo sapiens cytochrome P450 rethoid metabolizing protein P450RAI-2 mRNA, complete cds
4578	9694	14831	4.77	1.0E-127	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
4601	9716		2.3	1.0E-127	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4844	8762	14807	1.49	1.0E-127	6912839	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
459	5027	10767	2.94	1.0E-128	BE385617.1	EST_HUMAN	601278127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618822 5'
2063	7176	12417	80.69	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2063	7176	12418	80.69	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2181	7303	12553	172.11	1.0E-128	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
2422	7627		6.08	1.0E-128	11437455	NT	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3375	8520	13684	1.11	1.0E-128	AB033073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds
4824	9152	14899	5.88	1.0E-128	11426879	NT	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA
117	6680	10730	3.07	1.0E-128	S37722.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
412	5580	10730	3.48	1.0E-128	S37722.1	NT	Insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1733	6880	12063	5.33	1.0E-128	AL096880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
1737	6884	12087	1.65	1.0E-128	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1737	6884	12087	1.65	1.0E-128	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1737	6884	12087	1.65	1.0E-128	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
157	6977	12103	3.1	1.0E-129	11418522	NT	Homo sapiens zinc finger protein 78 (expressed in testis) (ZNF78), mRNA
3105	8258	13409	1.84	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3105	8258	13410	1.84	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3105	8258	13411	1.84	1.0E-129	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
4135	9283	14402	2.01	1.0E-129	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
4254	9379	14510	2.21	1.0E-129	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151835 similar to CMYA5
4254	9379	14511	2.21	1.0E-129	AW755254.1	EST_HUMAN	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151835 similar to CMYA5
75	6284	10423	2.24	1.0E-130	7705530	NT	Cardiomyopathy associated gene 5
1172	6307	11474	0.97	1.0E-130	AB037835.1	NT	Homo sapiens hypothetical protein (HSPC242), mRNA
1680	6809	12007	36.02	1.0E-130	BE276192.1	EST_HUMAN	Homo sapiens mRNA for KIAA1414 protein, partial cds
1680	6809	12008	36.02	1.0E-130	BE276192.1	EST_HUMAN	601121895F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346368 5'
1885	7102		2.3	1.0E-130	X04092.1	NT	601121895F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346368 5'
2733	7827		3.54	1.0E-130	AJ010230.1	NT	Human gene for catalase (EC 1.11.1.6) exon 8 mapping to chromosome 11, band p13
2844	7899	13187	1.29	1.0E-130	BE564219.1	EST_HUMAN	Homo sapiens RET finger protein-like 1 antisense transcript, partial
2844	7899	13188	1.29	1.0E-130	BE564219.1	EST_HUMAN	Homo sapiens RET finger protein-like 1 antisense transcript, partial
3563	8706	13887	0.8	1.0E-130	AF240888.1	NT	Homo sapiens cDNA clone IMAGE:3685468 5'
3748	7899	13157	5.45	1.0E-130	BE564219.1	EST_HUMAN	601343018F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685468 5'
3748	7899	13158	5.45	1.0E-130	BE564219.1	EST_HUMAN	601343018F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685468 5'
3909	9045	14204	1.33	1.0E-130	BE564219.1	EST_HUMAN	Homo sapiens retinol dehydrogenase homologue isoform-1 (RDH), complete cds
4048	9179	14320	0.92	1.0E-130	AW843893.1	EST_HUMAN	Homo sapiens retinol dehydrogenase homologue isoform-1 (RDH), complete cds
4511	9630	14774	0.92	1.0E-130	AW843893.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3078781 5'
5082	10183	15320	1.33	1.0E-130	AW363289.1	EST_HUMAN	UHPF-BNO-alky-g-08-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078781 5'
5082	10183	15321	1.33	1.0E-130	AW363289.1	EST_HUMAN	UHPF-BNO-alky-g-08-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078781 5'
5082	10183	15321	1.33	1.0E-130	AW363289.1	EST_HUMAN	Human T-cell receptor (V alpha 22.1, J alpha 1) mRNA
5082	10183	15321	1.33	1.0E-130	AW363289.1	EST_HUMAN	Human T-cell receptor (V alpha 22.1, J alpha 1) mRNA
5082	10183	15321	1.33	1.0E-130	AW363289.1	EST_HUMAN	CM4-CN0045-180200-511-002 CN0045 Homo sapiens cDNA
5082	10183	15321	1.33	1.0E-130	AW363289.1	EST_HUMAN	CM4-CN0045-180200-511-002 CN0045 Homo sapiens cDNA
5082	10183	15321	1.33	1.0E-130	AW363289.1	EST_HUMAN	RCO-CT0318-201199-031-ct11 CT0318 Homo sapiens cDNA
5082	10183	15321	1.33	1.0E-130	AW363289.1	EST_HUMAN	RCO-CT0318-201199-031-ct11 CT0318 Homo sapiens cDNA

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4	5216	10328	1.91	0.0E+00	AA228126.1	EST_HUMAN	z68c04.f1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:887680 5' similar to TR:G222811
4	5216	10329	1.91	0.0E+00	AA228126.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
7	5218	10332	3.34	0.0E+00	4885136	NT	z58c04.f1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:887680 5' similar to TR:G222811
14	5225	10337	1.38	0.0E+00	8923349	NT	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
14	5225	10338	1.38	0.0E+00	8923349	NT	Homo sapiens checkoint suppressor 1 (CHES1), mRNA
21	5232	10345	13.75	0.0E+00	D83327.1	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
21	5232	10346	13.75	0.0E+00	D83327.1	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
25	5236	10360	51.42	0.0E+00	AF141349.1	NT	Homo sapiens DORR1 mRNA, partial cds
33	5244	10360	1.99	0.0E+00	5802987	NT	Homo sapiens DORR1 mRNA, partial cds
35	5246	10363	0.77	0.0E+00	M69500.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
39	5250	10368	9.5	0.0E+00	6857825	NT	Homo sapiens Cdc42 effector protein 2 (CEP2), mRNA
58	5267	10395	12.92	0.0E+00	Y17151.2	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
58	5267	10396	12.92	0.0E+00	Y17151.2	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
58	5268	10400	6.88	0.0E+00	D78804.1	EST_HUMAN	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
58	5268	10401	6.88	0.0E+00	D78804.1	EST_HUMAN	HUM516H08B Human placenta polyA+ (TF-ujwara) Homo sapiens cDNA clone GEN-516H08 5'
59	5270	10402	37.3	0.0E+00	L16558.1	NT	HUM516H08B Human placenta polyA+ (TF-ujwara) Homo sapiens cDNA clone GEN-516H08 5'
61	5272	10405	13.22	0.0E+00	AW069534.1	EST_HUMAN	Human ribosomal protein L7 (RPL7) mRNA, complete cds
61	5272	10408	13.22	0.0E+00	AW069534.1	EST_HUMAN	cr48c07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48c07 3'
65	5275	10410	1.1	0.0E+00	M60678.1	NT	cr48c07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48c07 3'
68	5276	10421	0.79	0.0E+00	M60678.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
74	5283	10421	1.92	0.0E+00	4758977	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
74	5283	10422	1.92	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
78	5287	10427	0.72	0.0E+00	4501850	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
78	5288	10435	31.31	0.0E+00	4504444	NT	Homo sapiens epsilon-tubulin binding protein 1 (epsilon tubulin-binding) (ABP1), nuclear gene
87	5298	10435	84.52	0.0E+00	5016088	NT	encoding mitochondrial protein, mRNA
80	5298	10438	71.3	0.0E+00	U88277.1	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
97	5308	10445	4.27	0.0E+00	A1114743.1	EST_HUMAN	Homo sapiens actin, beta (ACTB) mRNA
98	5307	10446	1.52	0.0E+00	AB037784.1	NT	Human polyomavirus 1 homolog (HPV1) mRNA, partial cds
112	5316	10455	1.5	0.0E+00	A1823701.1	EST_HUMAN	HA1947 Human fetal liver cDNA library Homo sapiens cDNA
							Homo sapiens mRNA for KIAA1363 protein, partial cds
							ts48b05.x1 NC1_CQAP U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q89551 Q89551
							MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR ;

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
113	5316	10495	3.14	0.0E+00	AI623701.1	EST_HUMAN	ba38605.x1 NC1_QGAP_U14 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q89551 Q89551
114	7860	10456	4.61	0.0E+00	N36040.1	EST_HUMAN	MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR, ;
114	7860	10457	4.61	0.0E+00	N36040.1	EST_HUMAN	yo1109.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270017 6'
126	5324	10469	5.01	0.0E+00	45058368	NT	yo1109.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:270017 5'
126	5324	10470	5.01	0.0E+00	45058368	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220K0) (POLR2A) mRNA
134	5568	10714	1.62	0.0E+00	45058368	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220K0) (POLR2A) mRNA
136	5332	10477	1.43	0.0E+00	T6945.1	EST_HUMAN	Homo sapiens IgG Fc binding protein (FCGAMMA19P) mRNA
136	5332	10478	1.43	0.0E+00	T6945.1	EST_HUMAN	ya83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:58310 5'
148	6346	10491	24.18	0.0E+00	T6946.1	EST_HUMAN	ya83g04.r2 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:58310 5'
162	6349	10491	6.08	0.0E+00	BF039881.1	EST_HUMAN	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRP1) mRNA
164	5351	10491	83.85	0.0E+00	BF039881.1	EST_HUMAN	60114803.7F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3893903 5'
157	5354	10494	0.85	0.0E+00	AF111168.2	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRP1) mRNA
169	5368	10495	4.11	0.0E+00	BE285973.1	EST_HUMAN	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
160	5369	10496	3.81	0.0E+00	BE285973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'
161	5357	10496	7.12	0.0E+00	W73973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'
182	5368	10497	2.87	0.0E+00	BE162832.1	EST_HUMAN	z62805.r1 Soares_fetal_heart_NDHH19W Homo sapiens cDNA clone IMAGE:345201 5' similar to db:X16292_cds1 ZINC FINGER PROTEIN CLONE 847 (HUMAN);
182	5368	10498	2.87	0.0E+00	BE162832.1	EST_HUMAN	QV3-H10457-140200-088-404 HT0457 Homo sapiens cDNA
163	5369	10499	3.87	0.0E+00	AF244088.1	NT	QV3-H10457-140200-088-404 HT0457 Homo sapiens cDNA
169	5392	10502	57.01	0.0E+00	AL163202.2	NT	Homo sapiens zinc finger protein mRNA, complete cds
166	5392	10503	57.01	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
176	5370	10510	6.34	0.0E+00	BE018970.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C002
176	5370	10511	6.34	0.0E+00	BE018970.1	EST_HUMAN	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2868864 5' similar to WP:Y67A10A.Z
181	5376	10514	7.68	0.0E+00	AB018327.1	NT	OE22631 ;
181	5376	10516	7.68	0.0E+00	AB018327.1	NT	bb24e12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2868864 5' similar to WP:Y67A10A.Z
182	5376	10516	6.19	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
182	5376	10517	6.19	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
181	5368	10529	309.81	0.0E+00	D50859.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
186	5391	10534	13.52	0.0E+00	AF273045.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTG3P) pseudogene
186	5391	10535	13.52	0.0E+00	AF273045.1	NT	Homo sapiens GTC1 tumor antigen ae14-3 mRNA, complete cds
188	5393	10537	7.31	0.0E+00	AF167174.1	NT	Homo sapiens GTC1 tumor antigen ae14-3 mRNA, complete cds
188	5393	10537	7.31	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSJ3-2 protein mRNA, complete cds

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Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
198	5393	10538	7.31	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
207	7885	10544	27.02	0.0E+00	AI587308.1	EST_HUMAN	ig04f08.x1 NCI_CGAP_U03 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN 1 (HUMAN);
207	7885	10545	27.02	0.0E+00	AI587308.1	EST_HUMAN	ig04f08.x1 NCI_CGAP_U03 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN 1 (HUMAN);
209	6403	10547	2.59	0.0E+00	AF195858.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
212	6408		53.8	0.0E+00	4506832	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
213	6407		8.58	0.0E+00	AF132000.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
219	6413	10552	4.01	0.0E+00	AB018284.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
220	6413	10552	2.88	0.0E+00	AB018284.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
221	6414	10553	4.81	0.0E+00	6878444	NT	Mus musculus testis-specific protein, Y-encoded-like (Tspyl), mRNA
235	6428	10588	22.84	0.0E+00	5453805	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
237	6430		14.18	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21 C001
244	6435	10574	3.02	0.0E+00	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
246	6437	10577	1.02	0.0E+00	X89772.1	NT	H. sapiens mRNA for Interferon alpha/beta receptor (long form)
254	6445		6.18	0.0E+00	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
267	6457	10598	1.45	0.0E+00	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
267	6457	10597	1.45	0.0E+00	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
269	6459	10599	2.13	0.0E+00	7706028	NT	Homo sapiens hypothetical protein (LOC51250), mRNA
280	6469		4.7	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
281	6470	10612	5.27	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
281	6470	10613	5.27	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
282	6471		1.16	0.0E+00	AW84628.1	EST_HUMAN	IL2-CT0031-187188-020-803 CT0031 Homo sapiens cDNA
291	6479	10620	6.27	0.0E+00	4507029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
291	6479	10621	5.27	0.0E+00	4507029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
302	6490	10631	14.01	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
303	6491	10632	7.12	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
304	7888		24.79	0.0E+00	4508728	NT	Homo sapiens ribosomal protein S8 (RPS8) mRNA
305	6492	10633	0.93	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycylamide formyltransferase, phosphoribosylglycylamide synthetase, phosphoribosylaminimidazole synthetase (GART) mRNA
306	6493		3.88	0.0E+00	AA480002.1	EST_HUMAN	z18cd8.r1 Soares_NHMPRL_S1 Homo sapiens cDNA clone IMAGE:753894 5'
307	6494	10634	17.26	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
308	6494	10634	18.94	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
312	6498	10638	2.05	0.0E+00	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds

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Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
325	5510	10647	1.9	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (8TB AND CNC HOMOLOG 1) (HA2303)
326	5510	10648	1.9	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (8TB AND CNC HOMOLOG 1) (HA2303)
326	5511	10648	3.19	0.0E+00	7687213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
327	5511	10648	2.21	0.0E+00	7687213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
342	5525	10681	5.87	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
345	5528	10686	43.24	0.0E+00	4827057	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
348	5531	10670	2.56	0.0E+00	U71600.1	NT	Human zinc finger protein zfp31 (zfp31) mRNA, partial cds
353	5535	10674	2.88	0.0E+00	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
353	5535	10676	2.88	0.0E+00	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
354	7889	10678	2.95	0.0E+00	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
358	5537	10678	1.14	0.0E+00	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
359	5540	10682	1.84	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
360	5541	10683	2.71	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
361	5541	10683	2.65	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
363	5543	10695	1.05	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
374	5562	10698	4.43	0.0E+00	AU134863.1	EST_HUMAN	AU134863 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
385	5594	10740	7.76	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
386	5595	10741	2.53	0.0E+00	AJ353014.1	EST_HUMAN	q91h05.x1 NCLCGAP_Bm25 Homo sapiens cDNA clone IMAGE:2018457 3' similar to gb:X54189
397	5560	10703	4.73	0.0E+00	AW754160.1	EST_HUMAN	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (HUMAN);
394	5562	10708	2.69	0.0E+00	4503680	NT	RC2-CT0320-300100-018-408 CT0320 Homo sapiens cDNA
395	5563	10707	2.17	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
395	5563	10708	2.17	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
396	5564	10708	1.86	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
397	5565	10710	2.01	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
397	5565	10711	2.01	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
398	5566	10712	2.45	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
399	5567	10713	3.28	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
400	5568	10714	2.6	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
401	5569	10715	3.22	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
401	5569	10716	3.22	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
402	5569	10715	3.76	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
402	5569	10716	3.76	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
408	5573		752.9	0.0E+00	4506808	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
419	5208	10318	1.15	0.0E+00	R17795.1	EST_HUMAN	X03802.1 Soares Infant brain 1N18 Homo sapiens cDNA clone IMAGE31652 5'
427	5586	10742	1.21	0.0E+00	4503814	NT	Homo sapiens phosphoribosylglycylamide formyltransferase, phosphoribosylglycylamide synthetase, phosphoribosylaminimidazole synthetase (GART) mRNA
428	5597		20.02	0.0E+00	4503728	NT	Homo sapiens ribosomal protein S5 (RP-S5) mRNA
429	5588	10743	8.43	0.0E+00	AB028042.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
430	5599	10744	15.73	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
430	5599	10746	15.73	0.0E+00	4507162	NT	Homo sapiens SON DNA binding protein (SON) mRNA
431	5600	10746	8.04	0.0E+00	AF183607.1	NT	Mus musculus truncated SON protein (Son) mRNA, complete cds
443	5811		1.8	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
445	5813	10759	1.95	0.0E+00	4557878	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
450	5818		1.13	0.0E+00	AA324282.1	EST_HUMAN	EST127054 Carabellum II Homo sapiens cDNA 5' end
451	5819		1.64	0.0E+00	BE264447.1	EST_HUMAN	60111520F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE3352348 5'
467	5635	10773	3.39	0.0E+00	4504532	NT	Homo sapiens 5-hydroxycytoplamine (serotonin) receptor 1B (HTR1B) mRNA
467	5635	10774	3.39	0.0E+00	4504532	NT	Homo sapiens 5-hydroxycytoplamine (serotonin) receptor 1B (HTR1B) mRNA
473	5840	10782	55.72	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
473	5840	10783	55.72	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
483	5851	10789	4.42	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
484	5852	10790	5.18	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
484	5852	10791	6.18	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
485	5852	10798	3.45	0.0E+00	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
485	5852	10798	1.68	0.0E+00	AU132898.1	EST_HUMAN	AU132898 NT2RP4 Homo sapiens cDNA clone NT2RP4000837 5'
503	5870	10804	3.16	0.0E+00	BE385144.1	EST_HUMAN	60127495F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE3816768 5'
604	7892	10806	1.28	0.0E+00	AW898825.1	EST_HUMAN	PMO-DJ0065-130400-002-008 DT0065 Homo sapiens cDNA
607	5873	10807	2.7	0.0E+00	AL117233.1	NT	Novel human gene mapping to chromosome 1
608	5874	10808	1.29	0.0E+00	8923856	NT	Homo sapiens PC328 protein (PC328), mRNA
517	5893	10817	5.2	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
524	7893	10821	1.96	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0835-160400-142-h05 BT0835 Homo sapiens cDNA
529	5695	10827	1.37	0.0E+00	BF028005.1	EST_HUMAN	601784858F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE3808028 5'
536	5701	10834	2.3	0.0E+00	AB040809.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
538	5704	10837	19.21	0.0E+00	6006030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA
539	5705	10838	4.52	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
539	5705	10839	4.52	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
541	5707	10841	5.08	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
542	5708	10842	2.92	0.0E+00	8923831	NT	Homo sapiens enilin (LOC54443), mRNA
542	5708	10843	2.92	0.0E+00	8923831	NT	Homo sapiens enilin (LOC54443), mRNA
547	5712		5.28	0.0E+00	AF003528.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
555	5720	10852	2.09	0.0E+00	AW135324.1	EST_HUMAN	UI-H-B11-ecb-h-04-U1.s1 NC1 CGAP Sub3 Homo sapiens cDNA clone IMAGE:2713051 3'
555	5730		4.68	0.0E+00	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
584	5747	10876	4.19	0.0E+00	5174742	NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRCF1), nuclear gene encoding mitochondrial protein, mRNA
607	5769		3.99	0.0E+00	J04068.1	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1
600	5762	10880	2.17	0.0E+00	BF104898.1	EST_HUMAN	G018262F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045447 5'
606	5768	10894	0.67	0.0E+00	4501854	NT	Homo sapiens acyl-Coenzyme A carboxylase beta (ACACB), mRNA
611	5771	10900	1	0.0E+00	AF221742.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
611	5771	10901	1	0.0E+00	AF221742.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
621	5781	10911	2.78	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
623	5783	10914	2.3	0.0E+00	AB037807.1	NT	Homo sapiens mRNA for KIAA1368 protein, partial cds
625	5785	10916	1.54	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
626	5786	10918	1.9	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
626	5788	10917	1.9	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
627	5787	10918	0.89	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
627	5787	10919	0.89	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
634	5795	10929	1.16	0.0E+00	AA399486.1	EST_HUMAN	Z60007.1 Soares testis NHT Homo sapiens cDNA clone IMAGE:728732 5'
638	5799	10933	5.98	0.0E+00	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
642	5803	10936	0.67	0.0E+00	W78811.1	EST_HUMAN	zh51b04.1 Soares fetal liver, spleen, INFLS_81 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
642	5803	10937	0.67	0.0E+00	W78811.1	EST_HUMAN	zh51b04.1 Soares fetal liver, spleen, INFLS_81 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
645	5808		4.64	0.0E+00	4865528	NT	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA
652	5813	10949	2.56	0.0E+00	6006003	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
654	5815	10952	2	0.0E+00	5031624	NT	Homo sapiens CCAAT box-binding transcription factor (CBF2) mRNA
657	5818	10956	5.7	0.0E+00	U05235.1	NT	Human neutral amino acid transporter (ASCT1) gene, exon 8
661	5822	10959	0.8	0.0E+00	AF108398.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
661	5822	10960	0.8	0.0E+00	AF108399.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
667	5827	10965	4.98	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
667	5827	10968	4.68	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA

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Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
673	7888		2.1	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
681	5839	10979	18.62	0.0E+00	4504424	NT	Homo sapiens High-mobility group (nonhistone chromosomal) protein 1 (HMG1) mRNA
686	5843	10982	15.5	0.0E+00	AB028012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
685	5852	10987	3.84	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA np49307.s1 NCI_CGAP_B1.1 Homo sapiens cDNA clone IMAGE:1128333 3' similar to gb-X57352
707	5884	11011	7.47	0.0E+00	AA614537.1	EST_HUMAN	INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN);
711	5888	11016	5.35	0.0E+00	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
711	5888	11016	5.35	0.0E+00	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
721	5878	11026	1.28	0.0E+00	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
727	5883	11031	4.5	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
727	5883	11032	4.5	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
726	5885	11035	8.31	0.0E+00	11548800	NT	Homo sapiens hypothetical protein FLJ21834 (FLJ21834), mRNA
735	5891	11043	3.29	0.0E+00	BE241577.1	EST_HUMAN	TCAAP1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) Bayler-HGSC project-TCAA Homo sapiens cDNA clone TCAAP0779
755	5910	11087	0.87	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
755	5910	11088	0.87	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
768	5913	11071	0.77	0.0E+00	J03784.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
768	5913	11072	0.77	0.0E+00	J03784.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
761	5916	11073	2.26	0.0E+00	AB037760.1	NT	Homo sapiens mRNA for KIAA1339 protein, partial cds
762	5917	11074	3.68	0.0E+00	6912749	NT	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
704	7800	11076	4.44	0.0E+00	D30612.1	NT	Homo sapiens mRNA for repressor protein, partial cds
765	5918	11077	8.27	0.0E+00	BE869735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
769	5923	11081	3.65	0.0E+00	R48915.1	EST_HUMAN	X65908.1 Soares breast 2NHBst Homo sapiens cDNA clone IMAGE:154046 5'
770	5924	11082	9.85	0.0E+00	6032086	NT	Homo sapiens splicing factor 3a, subunit 1, 120KD (SF3A1), mRNA
779	5933	11091	2.28	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
782	5937	11095	4.63	0.0E+00	7661688	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
783	5947	11107	1.45	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
783	5947	11108	1.45	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
788	5952	11112	1.09	0.0E+00	X89772.1	NT	H. sapiens mRNA for interferon alpha/beta receptor (long form)
802	5956	11116	2.27	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0810 protein, partial cds
802	5956	11117	2.27	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0810 protein, partial cds
807	5960	11123	7.36	0.0E+00	5174478	NT	Homo sapiens pericentriin (PCNT) mRNA
808	5961		7.7	0.0E+00	4507600	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
825	5978	11144	1.77	0.0E+00	7667213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
828	5979	11145	2.22	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
828	5981	11147	2.39	0.0E+00	4557898	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 1 (KCNE1), mRNA
834	5986	11183	1.75	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH), mRNA, complete cds
834	5986	11154	1.75	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH), mRNA, complete cds
835	5987	11189	0.94	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH), mRNA, complete cds
840	5982	11160	2.02	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
844	5995	11185	1.79	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
844	5995	11186	1.79	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
851	6002	11177	1.87	0.0E+00	AF027153.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3), gene, complete cds
855	6003	11177	6.75	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
855	6003	11178	6.75	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
856	6007	11179	14.37	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON), mRNA
857	6008	11180	9.8	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
858	6009	11181	12.33	0.0E+00	4508728	NT	Homo sapiens ribosomal protein S6 (RPS6), mRNA
862	6013	11184	1.11	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
862	6013	11185	1.11	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
863	6014	11188	1.69	0.0E+00	AA533272.1	EST_HUMAN	U88407 s1 NC1_CGAP_P10 Homo sapiens cDNA clone IMAGE:597453
863	6014	11187	1.69	0.0E+00	AA533272.1	EST_HUMAN	U88407 s1 NC1_CGAP_P10 Homo sapiens cDNA clone IMAGE:597453
864	6015	11187	5.77	0.0E+00	BF977894.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'
868	6019	11188	1.57	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
868	6019	11189	1.57	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
869	6020	11190	1.83	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
869	6020	11191	1.83	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
892	6042	11214	0.99	0.0E+00	AL163203.2	NT	Homo sapiens chitinase 21 segment HS21C0003
899	6049	11219	1.47	0.0E+00	BE08992.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
899	6049	11220	1.47	0.0E+00	BE08992.1	EST_HUMAN	QV0-BT0703-280400-211-g11 BT0703 Homo sapiens cDNA
909	6059	11229	3.59	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C0003
918	6067	11230	28.71	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
921	6067	11230	23.9	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
922	6070	11236	1	0.0E+00	AF089747.1	NT	Homo sapiens alpha-1-antitrypsin precursor, mRNA, partial cds
923	6071	11237	0.75	0.0E+00	S69384.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
923	6071	11238	0.75	0.0E+00	S69384.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
923	6071	11239	0.75	0.0E+00	S69384.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
924	6072	11240	1.69	0.0E+00	L28101.1	NT	Homo sapiens kallistatin (P14) gene, exons 1-4, complete cds

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827	6076	11243	4.57	0.0E+00	Z20686.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
827	6076	11244	4.57	0.0E+00	Z20686.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
847	6086	11262	2.02	0.0E+00	AB028211.1	NT	Homo sapiens mRNA for KIAA0894 protein, partial cds
847	6086	11263	2.02	0.0E+00	AB028211.1	NT	Homo sapiens mRNA for KIAA0894 protein, partial cds
952	6100	11268	1.26	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
953	6101	11269	6.7	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
954	6102	11270	0.79	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
955	6103	11271	2.01	0.0E+00	4507430	NT	Homo sapiens thymocyte embryonic factor (TEF), mRNA
955	6103	11272	2.01	0.0E+00	4507430	NT	Homo sapiens thymocyte embryonic factor (TEF), mRNA
953	7805	11279	2.13	0.0E+00	A001948.1	EST_HUMAN	os88e03.s1 NCL CGAP_GCS Homo sapiens cDNA clone IMAGE:1613404 3'
953	7805	11280	2.13	0.0E+00	A001948.1	EST_HUMAN	os88e03.s1 NCL CGAP_GCS Homo sapiens cDNA clone IMAGE:1613404 3'
955	6112	11282	11.65	0.0E+00	7657266	NT	Homo sapiens KIAA0928 protein Mex2 interacting nuclear target (MINT) homolog (KIAA0928), mRNA
979	6122	11282	1.42	0.0E+00	AB030566.1	NT	Homo sapiens mRNA for PSP24, complete cds
984	6130	11298	1.57	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050800-001-402 GN0014 Homo sapiens cDNA
984	6130	11299	1.57	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050800-001-402 GN0014 Homo sapiens cDNA
984	6130	11300	1.57	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050800-001-402 GN0014 Homo sapiens cDNA
985	6131	11301	1.52	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
985	6131	11302	1.52	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
984	6140	11309	6.89	0.0E+00	4757869	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
1005	6150	11317	1.56	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4c) gene, complete cds
1006	6151	11318	37.21	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4c) gene, complete cds
1007	6151	11318	22.91	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4c) gene, complete cds
1010	6154		4.81	0.0E+00	AF108480.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1011	6154		9.74	0.0E+00	AF108480.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1016	6158	11324	2.06	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1016	6158	11324	3.94	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1017	6159	11324	3.21	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1018	6159	11325	4.91	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1021	6162	11326	2.38	0.0E+00	7691695	NT	Homo sapiens DKFZP686K0122 protein (DKFZP686K0122), mRNA
1026	6166	11332	3.69	0.0E+00	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1027	6168		4.4	0.0E+00	AA458680.1	EST_HUMAN	aa86p07.s1 Stragene fetal refseq 837202 Homo sapiens cDNA clone IMAGE:838236 3' similar to SW:PR58_HUMAN P47210 28S PROTEASE REGULATORY SUBUNIT 8;

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1030	6171	11337	7.44	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1030	6171	11338	7.44	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 51124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1031	6172	11339	1.27	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1031	6172	11340	1.27	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1031	6172	11340	1.27	0.0E+00	8922633	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1038	6176		2.42	0.0E+00	8922633	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1049	6180	11355	10.11	0.0E+00	4768669	NT	Homo sapiens heat shock 70kD protein 8B (morillin-2) (HSPA8B) mRNA
1068	6206	11388	2.38	0.0E+00	4826672	NT	Homo sapiens cadherin 8, K-cadherin (fetal kidney) (CDH6) mRNA
1068	6206	11388	2.38	0.0E+00	4826672	NT	Homo sapiens cadherin 8, K-cadherin (fetal kidney) (CDH6) mRNA
1070	6210	11373	2.8	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1070	6210	11373	2.8	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1070	6210	11374	2.8	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1071	6211	11375	68.12	0.0E+00	A1245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1073	6213		2.44	0.0E+00	6923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1073	6213	11378	2.44	0.0E+00	6923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1073	6213	11378	2.44	0.0E+00	5174384	NT	Homo sapiens alkylation repair; alkB homolog (ABH), mRNA
1073	6213	11378	2.44	0.0E+00	5174384	NT	Homo sapiens alkylation repair; alkB homolog (ABH), mRNA
1083	6222	11389	4.61	0.0E+00	4758117	NT	Homo sapiens Death associated protein 3 (DAP3) mRNA
1083	6222	11389	4.61	0.0E+00	BE005208.1	EST_HUMAN	MRO-BN0115-200300-003-H08 BN0115 Homo sapiens cDNA
1087	6235	11398	2.69	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 8 (KCNK8), mRNA
1120	6258	11422	5.21	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 8 (KCNK8), mRNA
1120	6258	11423	5.21	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1133	6270	11433	2.38	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1133	6270	11434	2.38	0.0E+00	4506712	NT	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
1134	6271	11435	20.33	0.0E+00	4506712	NT	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
1138	6273	11437	1.6	0.0E+00	8923260	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1139	6276	11440	16.73	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1141	6278	11441	52.48	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1142	6278	11442	5.53	0.0E+00	7657488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L), mRNA
1142	6278	11443	5.53	0.0E+00	7657488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L), mRNA
1148	6282	11448	2.67	0.0E+00	7706500	NT	Homo sapiens Npw38-binding protein Npw38P (LOC61728), mRNA
1147	6283	11447	0.7	0.0E+00	X95928.1	NT	Homo sapiens ART4 gene
1147	6283	11448	0.7	0.0E+00	X95928.1	NT	Homo sapiens ART4 gene
1147	6283	11448	0.7	0.0E+00	X95928.1	NT	Homo sapiens ART4 gene
1148	6284	11448	1.44	0.0E+00	A1147650.1	EST_HUMAN	q22d10.x1 Scores_pregnant_uterus_NibHPU Homo sapiens cDNA clone IMAGE:10970113
1150	6286	11451	1.59	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1157	6283	11457	1.11	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1157	6283	11458	1.11	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA

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1168	6294	11459	0.9	0.0E+00	6868844	NT	Homo sapiens chromosome 12 open reading frame 3 (G12ORF3), mRNA
1170	6305	11471	3.47	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brn, 67KD) (GAD1), transcript variant GAD25, mRNA
1170	6305	11472	3.47	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brn, 67KD) (GAD1), transcript variant GAD25, mRNA
1173	6308	11476	1.84	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1180	6315	11484	51.8	0.0E+00	4557687	NT	Homo sapiens keratin 18 (KRT18), mRNA
1184	6328	11495	2.36	0.0E+00	AF073289.1	NT	Homo sapiens Nax/H+ exchanger isoform 2 (NHE2), mRNA, complete cds
1212	6344		1.73	0.0E+00	7857338	NT	Homo sapiens miR-1 (E. coli) homolog 3 (MLH3), mRNA
1225	6357	11527	1.26	0.0E+00	8922583	NT	Homo sapiens hypodermal protein FLJ10697 (FLJ10697), mRNA
1229	6361	11631	3.23	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1229	6361	11632	3.23	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1230	6362	11533	5.19	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1231	7911	11534	4.17	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1250	6380	11559	8.44	0.0E+00	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1251	6381	11560	1.11	0.0E+00	4503068	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1261	6390	11566	10.12	0.0E+00	4505740	NT	Homo sapiens prefoldin 4 (PFDN4), mRNA
1270	6399		2.69	0.0E+00	Y18000.1	NT	Homo sapiens NF2 gene
1278	6407	11681	181.34	0.0E+00	4508718	NT	Homo sapiens ribosomal protein S2 (RPS2), mRNA
1285	6414	11590	5.41	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCR9), mRNA, complete cds
1291	6420	11594	2.8	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1291	6420	11595	2.8	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1304	6434	11609	2.48	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS), mRNA
1304	6434	11610	2.48	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS), mRNA
1305	6435		2.72	0.0E+00	AF089156.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 5
1316	7913	11622	1.16	0.0E+00	7857629	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1316	7913	11623	1.16	0.0E+00	7857629	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1321	6460	11620	1.16	0.0E+00	6803146	NT	Homo sapiens ring finger protein 173 (ZNF173), mRNA
1322	6451	11630	3.29	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173), mRNA
1324	6453	11631	1.01	0.0E+00	6803146	NT	Homo sapiens zinc finger protein 173 (ZNF173), mRNA
1325	6454	11632	2.76	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173), mRNA
1327	6456	11634	4.1	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1328	6457	11635	7.17	0.0E+00	7661865	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1329	6458	11636	4.33	0.0E+00	7661865	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1330	6459	11637	4.06	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1330	6459	11638	4.08	0.0E+00	8587387	NT	Homo sapiens perlecan (Drosophila) homolog 3 (PER3), mRNA
1342	6470	11651	2.07	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
1416	6543	11722	0.98	0.0E+00	AJ250014.1	NT	Homo sapiens mRNA for Familial Cylindromatosis cycl gene
1422	6549	11730	5.33	0.0E+00	AJ277692.1	NT	Homo sapiens partial TTN gene for titin
1425	6552	11734	1.43	0.0E+00	AI208758.1	EST_HUMAN	cg38508.x1 Scaree3 _{antisense} NHT Homo sapiens cDNA clone IMAGE:1837427 3' similar to WP:T27A1.5
1428	6553	11735	22.77	0.0E+00	6042208	NT	RAN, member RAS oncogene family/Homo sapiens RAN, member RAS oncogene family (RAN), mRNA
1435	6562	11745	2.3	0.0E+00	4505546	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1436	6562	11746	2.3	0.0E+00	4505548	NT	Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1437	6584	11749	4.16	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1437	6584	11750	4.16	0.0E+00	7705566	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1440	6567	11762	4.87	0.0E+00	AJ238093.1	NT	Homo sapiens partial AIF-4 gene, exons 2 to 7 and Alu repeat elements
1450	6576	11765	4.23	0.0E+00	AF038280.1	NT	Homo sapiens alpha1-D-glucosyltransferase (alpha1-GT) gene, exon 7
1461	6588	11777	2.18	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1468	6593	11781	4.88	0.0E+00	U36637.1	NT	Human nebulin mRNA, partial cds
1468	6593	11782	4.88	0.0E+00	U36637.1	NT	Human nebulin mRNA, partial cds
1474	6601	11786	2.57	0.0E+00	AL132989.1	NT	Novel human gene on chromosome 20
1476	6602	11787	1.36	0.0E+00	AL137784.1	NT	Novel human gene mapping to chromosome 1
1478	6606	11792	1.8	0.0E+00	D87077.1	NT	Human mRNA for KIAA0240 gene, partial cds
1482	6609	11795	6.7	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1484	6811	11797	1.25	0.0E+00	7681865	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1484	6811	11798	1.25	0.0E+00	7681865	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1525	6652	11838	1.35	0.0E+00	7706434	NT	Homo sapiens HHD for homolog of Drosophila headcase (LOC31688), mRNA
1539	6687	11853	1.51	0.0E+00	AW859687.1	EST_HUMAN	EST T371757 MAGC resequences, MAGF Homo sapiens cDNA
1540	6688	11854	2.48	0.0E+00	AA481172.1	EST_HUMAN	aa34403.1 NCI_OGAP_GCB1 Homo sapiens cDNA clone IMAGE:815118 5'
1546	6674	11858	130.24	0.0E+00	AF023860.1	NT	Carcinophilus aethiops cyclophilin A mRNA, complete cds
1548	6874	11859	130.24	0.0E+00	AF023860.1	NT	Carcinophilus aethiops cyclophilin A mRNA, complete cds
1548	6876	11862	1.27	0.0E+00	AW979037.1	EST_HUMAN	EST T388208 MAGC resequences, MAGN Homo sapiens cDNA
1548	6876	11863	1.27	0.0E+00	AW979037.1	EST_HUMAN	EST T388208 MAGC resequences, MAGN Homo sapiens cDNA
1549	6877	11864	2.41	0.0E+00	D10884.1	NT	Bovine mRNA for neurocalcin
1551	6878		2.42	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosylase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1552	6881	11868	5.69	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1552	6981	11869	5.69	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA
1553	6882	11870	2.73	0.0E+00	7682405	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
1554	6883		7.14	0.0E+00	7656372	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1560	6889	11876	3.37	0.0E+00	M88478.1	NT	Human transglutaminase mRNA, complete cds
1563	6892	11878	2.36	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1563	6892	11878	2.36	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1584	7920		48.36	0.0E+00	4506854	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
1565	6893	11880	42.77	0.0E+00	M14189.1	NT	Human laminin receptor (246 epitope) mRNA, 5' end
1576	6705	11895	2.22	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1576	6705	11896	2.22	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1578	6707	11897	6.89	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (maternal-associated) (CSPG4), mRNA
1584	6713		3.79	0.0E+00	D00333.1	NT	human c-yes-2 gene
1584	6722	11912	11.87	0.0E+00	Z83738.1	NT	H. sapiens hH2Ble gene
1594	6723	11913	1.35	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1594	6723	11914	1.35	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1596	6724	11916	7.46	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKCG Homo sapiens cDNA clone GKCB0F02 6'
1595	6724	11918	7.45	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKCG Homo sapiens cDNA clone GKCB0F02 5'
1598	7921	11919	6.37	0.0E+00	AB040905.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1601	6729	11920	1.64	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1603	6731	11923	6.11	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1603	6731	11924	6.11	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1605	6733	11925	108.24	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1605	6733	11926	108.24	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1607	6736	11928	2.08	0.0E+00	M91803.1	NT	Human sodium channel mRNA
1622	6750	11944	8.74	0.0E+00	H26873.1	EST_HUMAN	yo78605.s1 Soares adult brain N2b-4HB55Y Homo sapiens cDNA clone IMAGE:183848 3'
1630	6768	11964	2.1	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1630	6769	11965	2.1	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1648	6777	11969	1.69	0.0E+00	AW444637.1	EST_HUMAN	UHHBIS-gw-c-04-QJL1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:2733284 3'
1678	6807	12004	1.53	0.0E+00	BE144364.1	EST_HUMAN	MRD-HT0168-191169-004-b11 HT0168 Homo sapiens cDNA
1678	6807	12005	1.53	0.0E+00	BE144364.1	EST_HUMAN	MRD-HT0168-191169-004-b11 HT0168 Homo sapiens cDNA
							W81807.x1 Soares NSF F8_9W_OT_PA_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to
1682	6811	12009	2.67	0.0E+00	A1768104.1	EST_HUMAN	TR-Q82788 Q82788 CYS2HIS2 ZINC FINGER PROTEIN. ;
1683	6812	12010	1.99	0.0E+00	4758513	NT	Homo sapiens hematopoietic-derived zinc finger protein (HD-ZNF1) mRNA

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1684	6813	12011	2.16	0.0E+00	AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
1687	6816	12014	3.33	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1687	6816	12014	3.33	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1689	6818	12017	46.16	0.0E+00	4657887	NT	Human seipin keratin 18 (KRT18) mRNA
1690	6819	12018	1	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
1694	6823	12021	1.5	0.0E+00	BE222374.1	EST_HUMAN	Hu11d05.x1 NC1 CGAP Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:095147 095147
1694	6823	12022	1.5	0.0E+00	BE222374.1	EST_HUMAN	HKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1698	6824	12024	1.76	0.0E+00	4557810	NT	HKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1699	6827	12027	6.05	0.0E+00	HS01932.1	EST_HUMAN	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1699	6827	12028	5.05	0.0E+00	HS01932.1	EST_HUMAN	Y69608.r1 Scores breast 3NH-Bst Homo sapiens cDNA clone IMAGE:182248 5' similar to gb:M84099
1701	6828	12030	10.76	0.0E+00	Z80780.1	NT	GAMMA-GLUTAMYLTRANSFERASE 5 PRECURSOR (HUMAN);
1701	6828	12031	10.76	0.0E+00	Z80780.1	NT	GAMMA-GLUTAMYLTRANSFERASE 5 PRECURSOR (HUMAN);
1704	6832	12041	37.89	0.0E+00	5031748	NT	H. sapiens H2B/h gene
1712	6840	12041	1.57	0.0E+00	AF169863.1	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMGP17), mRNA
1714	6841	12044	4.76	0.0E+00	8923841	NT	Homo sapiens WNT16 protein (WNT16) mRNA, complete cds
1717	6844	12047	1.8	0.0E+00	5453856	NT	Homo sapiens FOXJ2 forkhead factor (LOC55810), mRNA
1722	6849	12054	1.39	0.0E+00	4826979	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
1728	6855	12061	6.89	0.0E+00	AB026542.1	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMY1A1) mRNA
1730	6857	12061	1.94	0.0E+00	S94400.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
1744	7824	12076	1.21	0.0E+00	11645911	NT	TCR zeta [human, Genbank/mRNA, 365 nt, segment 1 of 8]
1757	6883	12080	2.79	0.0E+00	AF273841.1	NT	Homo sapiens NOD2 protein (NOD2), mRNA
1765	7826	12080	97	0.0E+00	4609718	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1800	6825	12138	2.59	0.0E+00	4557558	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1800	6825	12137	2.96	0.0E+00	4557558	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1803	6827	12141	2.04	0.0E+00	U63963.1	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1807	6931	12141	1.14	0.0E+00	W78571.1	EST_HUMAN	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1808	7828	12148	6.37	0.0E+00	4606332	NT	z686g03.r1 Scores_fetal_heart_NH-H19W Homo sapiens cDNA clone IMAGE:245584 5'
1819	6942	12180	21.49	0.0E+00	U14987.1	NT	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA
1821	6944	12163	19.15	0.0E+00	AB002331.1	NT	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA
1821	6944	12163	19.15	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds

Single Exon Probes Expressed In BT474

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1822	6945	12104	25.6	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1822	6945	12105	25.6	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1822	6945	12106	25.6	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1836	6958	12181	2.33	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1836	6958	12182	2.33	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1848	6969	12189	4.05	0.0E+00	6006655	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1848	6969	12190	4.05	0.0E+00	6006655	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1855	6976	12197	2.57	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1855	6976	12198	2.57	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1859	6979	12200	3.45	0.0E+00	4926783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1859	6979	12201	3.45	0.0E+00	4926783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1860	6980	12202	6.38	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1860	6980	12203	6.38	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1863	6983	12206	4.21	0.0E+00	AW207280.1	EST_HUMAN	UHH-B11-afn-4-07-Q-U1.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1863	6983	12207	4.21	0.0E+00	AW207280.1	EST_HUMAN	UHH-B11-afn-4-07-Q-U1.s1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1885	7005	12224	3.11	0.0E+00	BE277485.1	EST_HUMAN	601178164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1885	7005	12225	3.11	0.0E+00	BE277485.1	EST_HUMAN	601178164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1801	7020	12240	1.4	0.0E+00	BE006292.1	EST_HUMAN	RC2-BN0128-200300-012-b04 BN0128 Homo sapiens cDNA
1825	7044	12284	1.89	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1825	7044	12285	1.89	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220), mRNA
1828	7047	12287	3.05	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1828	7047	12288	3.05	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1833	7052	12274	2.16	0.0E+00	AB037788.1	NT	Homo sapiens mRNA for KIAA1367 protein, partial cds
1836	7055		1.49	0.0E+00	AF157478.1	NT	Homo sapiens DNA polymerase beta catalytic subunit (REV3) mRNA, complete cds
1941	7060	12283	3.37	0.0E+00	4507484	NT	Homo sapiens transforming growth factor, beta 3 (TGF-beta3), mRNA
1941	7060	12284	3.37	0.0E+00	4507484	NT	Homo sapiens transforming growth factor, beta 3 (TGF-beta3), mRNA
1944	7082	12286	1.05	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
1946	7084		6.43	0.0E+00	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

Single Exon Probes Expressed In BT474

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1961	7069		2.25	0.0E+00	M55632.1	NT	Human topoisomerase I pseudogene 1
1962	7080	12363	1.2	0.0E+00	5901805	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA
1964	7071	12296	1.08	0.0E+00	BE018069.1	EST_HUMAN	b57311.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048048 6'
1966	7077	12300	1.49	0.0E+00	4809282	NT	Homo sapiens histidine aminotransferase (HAL) mRNA
1966	7077	12301	1.49	0.0E+00	4809282	NT	Homo sapiens histidine aminotransferase (HAL) mRNA
1971	7088	12315	2.57	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1971	7088	12316	2.57	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
1972	7089	12317	10.13	0.0E+00	4826639	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1972	7089	12318	10.13	0.0E+00	4826639	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1982	7099	12330	1.53	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0780 protein, partial cds
1982	7099	12331	1.53	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0780 protein, partial cds
1987	7104	12335	1.16	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
1987	7104	12336	1.16	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
1989	7106	12337	3.18	0.0E+00	AW18024.1	EST_HUMAN	AB0501.x1 NCI_CGAP_Pari Homo sapiens cDNA clone IMAGE:2878913 3'
1989	7106	12338	3.18	0.0E+00	AW18024.1	EST_HUMAN	AB0501.x1 NCI_CGAP_Pari Homo sapiens cDNA clone IMAGE:2878913 3'
1990	7107	12339	6.81	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1990	7107	12340	6.81	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1992	7109	12342	1.01	0.0E+00	7682098	NT	Homo sapiens KIAA0408 gene product (KIAA0408), mRNA
1993	7110	12343	1.8	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
1994	7111	12344	1.53	0.0E+00	Z47550.1	NT	H sapiens genes for semenogelin I and semenogelin II
1994	7111	12345	1.53	0.0E+00	Z47550.1	NT	H sapiens genes for semenogelin I and semenogelin II
2001	7118	12354	5.38	0.0E+00	AB010948.1	NT	Homo sapiens mRNA for KIAA1613 protein, partial cds
2016	7133	12370	1.75	0.0E+00	AF273941.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2016	7133	12371	1.75	0.0E+00	AF273941.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2043	7181	12400	1.13	0.0E+00	7708742	NT	Homo sapiens TP53TG3a (TP53TG3a), mRNA
2049	7166	12404	23.48	0.0E+00	BE743215.1	EST_HUMAN	601673895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835188 6'
2048	7165	12405	23.48	0.0E+00	BE743215.1	EST_HUMAN	601673895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835188 6'
							Homo sapiens coagulation factor IX (plasma thrombopoietic component, Christmas disease, hemophilia B) (F9) mRNA
2051	7187	12408	1.37	0.0E+00	4503648	NT	
2052	7188	12407	2.16	0.0E+00	BF207988.1	EST_HUMAN	601861874F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:4081483 6'
2053	7168	12408	3.63	0.0E+00	AU140831	EST_HUMAN	AU140831 PLACE4 Homo sapiens cDNA clone PLACE4000321 5'
2055	7171	12410	1.56	0.0E+00	AA077989.1	EST_HUMAN	7822E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7822E10
2056	7171	12411	1.56	0.0E+00	AA077989.1	EST_HUMAN	7822E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7822E10
2057	7173		1.8	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA

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Table 4

Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2059	7175		1.25	0.0E+00	4585853	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2060	7176	12414	1.78	0.0E+00	Z42389.1	EST_HUMAN	HSC01C021 normalized infant brain cDNA Homo sapiens cDNA clone c-01c02
2062	7178		1.1	0.0E+00	A1244247.1	EST_HUMAN	q96068.x1 NCI_CGAP_U02 Homo sapiens cDNA clone IMAGE:1888871 3' similar to contains Alu repetitive element
2066	7182	12422	2.39	0.0E+00	BE87723.1	EST_HUMAN	601485149F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887747 5'
2088	7184	12424	2.08	0.0E+00	BF315325.1	EST_HUMAN	601802604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2089	7184	12425	2.08	0.0E+00	BF315325.1	EST_HUMAN	601802604F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2073	7189	12431	2.66	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2073	7189	12432	2.68	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2079	7185	12439	2.02	0.0E+00	L08820.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2079	7185	12440	2.02	0.0E+00	L08820.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2080	7186	12441	1.02	0.0E+00	AJ297708.1	NT	Homo sapiens mRNA for CDC2L5 protein kinase, (CDC2L5 gene), isoform 1
2083	7189	12444	1.6	0.0E+00	4758480	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2103	7218		3.19	0.0E+00	BE767884.1	EST_HUMAN	QV1-GN0065-149800-318-d10 GN0065 Homo sapiens cDNA
2104	7218		1.48	0.0E+00	AF018963.1	NT	Homo sapiens X-linked juvenile retinoschisis protein (XLRIS1) gene, exon 8 and complete cds
2106	7221	12485	6.48	0.0E+00	BF027662.1	EST_HUMAN	601872068F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3854785 5'
2107	7222	12488	1.85	0.0E+00	BE072624.1	EST_HUMAN	PMO-BT0547-210300-004-F04 BT0547 Homo sapiens cDNA
2109	7224	12487	2.8	0.0E+00	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2112	7227	12469	6.06	0.0E+00	AW762708.1	EST_HUMAN	IL3-CT0219-271099-022-G10 CT0219 Homo sapiens cDNA
2113	7228	12470	1.02	0.0E+00	L76627.1	NT	Homo sapiens metabotropic glutamate receptor 1 alpha (mGluR1 alpha) mRNA, complete cds
2115	7230	12472	10.82	0.0E+00	A1804640.1	EST_HUMAN	QV-BT065-020389-092 BT065 Homo sapiens cDNA
2115	7230	12473	10.82	0.0E+00	A1804640.1	EST_HUMAN	QV-BT065-020389-092 BT065 Homo sapiens cDNA
2161	7274		2.02	0.0E+00	L14787.1	NT	Human DNA-binding protein mRNA, 3' end
2168	7281	12527	1.29	0.0E+00	BE274688.1	EST_HUMAN	601122338F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346888 5'
2170	7283	12530	1.18	0.0E+00	DB7885.1	NT	Human mRNA for KIAA0244 gene, partial cds
2171	7284	12531	47.78	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBINDE08 5'
2171	7284	12532	47.78	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBINDE08 5'
2173	7286	12534	20.57	0.0E+00	AA831691.1	EST_HUMAN	cc32401.s1 NCI_CGAP_L05 Homo sapiens cDNA clone IMAGE:1667888 3'
2175	7288		1.32	0.0E+00	M19828.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 22 through 28
2178	7281	12538	8.02	0.0E+00	BF344434.1	EST_HUMAN	602014820F1 NCI_CGAP_Bim4 Homo sapiens cDNA clone IMAGE:4150734 5'
2179	7282	12539	143.71	0.0E+00	BE748899.1	EST_HUMAN	601572186F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3839012 3'
2183	7286	12543	2.92	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA
2183	7286	12544	2.92	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-508 TN0141 Homo sapiens cDNA

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2186	7305	12547	7.23	0.0E+00	BF313617.1	EST_HUMAN	601800281F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126822 5'
2189	7301	12550	2.24	0.0E+00	BE018760.1	EST_HUMAN	601800281F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR:Q15170 Q15170
2190	7302	12551	2.88	0.0E+00	AA042813.1	EST_HUMAN	TRANSCRIPTION FACTOR SII-RELATED PROTEIN ; 263607.s1 Soares_pregnant_uterus_NbHPJ Homo sapiens cDNA clone IMAGE:468540 3' similar to 601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2190	7302	12562	2.98	0.0E+00	AA042813.1	EST_HUMAN	TRANSCRIPTION FACTOR SII-RELATED PROTEIN ; 263607.s1 Soares_pregnant_uterus_NbHPJ Homo sapiens cDNA clone IMAGE:468540 3' similar to
2197	7309	12559	3.51	0.0E+00	AL163204.2	NT	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2197	7309	12560	3.51	0.0E+00	AL163204.2	NT	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2198	7310	12561	3.77	0.0E+00	7682401	NT	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2198	7310	12562	3.77	0.0E+00	7682401	NT	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2203	7315	12572	2.39	0.0E+00	U36284.1	NT	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2210	7322	12572	6.18	0.0E+00	BE897487.1	EST_HUMAN	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2222	7334	12583	6.73	0.0E+00	4557568	NT	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2227	7339	12583	1.81	0.0E+00	7682401	NT	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2233	7345	12600	4.45	0.0E+00	BE895281.1	EST_HUMAN	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2237	7349	12604	2.4	0.0E+00	BE905663.1	EST_HUMAN	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2237	7349	12605	2.4	0.0E+00	BE905663.1	EST_HUMAN	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2239	7350	12607	2.92	0.0E+00	AB037784.1	NT	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2274	7394	12632	3.79	0.0E+00	BF344766.1	EST_HUMAN	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2274	7394	12633	3.79	0.0E+00	BF344766.1	EST_HUMAN	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2276	7396	12635	3.08	0.0E+00	11545748	NT	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2276	7396	12636	3.08	0.0E+00	11545748	NT	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2277	7397	12637	2.9	0.0E+00	AI076404.1	EST_HUMAN	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2280	7390	12640	3.55	0.0E+00	AA428001.1	EST_HUMAN	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2280	7390	12641	3.55	0.0E+00	AA428001.1	EST_HUMAN	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2282	7392	12643	2.98	0.0E+00	BF347039.1	EST_HUMAN	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2283	6880	11867	1.1	0.0E+00	M19768.1	NT	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2288	7397	12649	1.03	0.0E+00	L02840.1	NT	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2289	7398	12650	1.01	0.0E+00	AB020717.1	NT	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2289	7398	12651	1.01	0.0E+00	AB020717.1	NT	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2290	7398	12652	1.23	0.0E+00	6325466	NT	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to
2297	7406	12658	2.88	0.0E+00	BE976095.1	EST_HUMAN	601800281F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:468540 3' similar to

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Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2300	7409	12680	11.14	0.0E+00	AF044571.1	NT	Homo sapiens phosphatase kinase alpha subunit (PHKA2) gene, exon 32
2301	7410	12681	1.94	0.0E+00	AB25542.1	EST_HUMAN	p47cd8.x1 NC1 CGAP_U12 Homo sapiens cDNA clone IMAGE:2283182 3'
2303	7412	12682	1.89	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
2305	7415	12684	3.71	0.0E+00	7682401	NT	Homo sapiens KIAA0852 protein (KIAA0852), mRNA
2306	7415	12685	3.71	0.0E+00	7682401	NT	Homo sapiens KIAA0852 protein (KIAA0852), mRNA
2308	7418	12688	2.32	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2309	7418	12689	2.32	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2316	7424	12674	1.92	0.0E+00	7682007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2316	7424	12675	1.92	0.0E+00	7682007	NT	Homo sapiens KIAA0218 gene product (KIAA0218), mRNA
2320	7428	12680	1.25	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2320	7428	12681	1.25	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2328	7438	12688	1.8	0.0E+00	5174678	NT	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA
2332	7439	12692	2.97	0.0E+00	AU131142.1	EST_HUMAN	AU131142 NT2RP3 Homo sapiens cDNA clone NT2RP3002084 5'
2333	7440	12693	70.49	0.0E+00	BE794028.1	EST_HUMAN	60168843F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941003 5'
2334	7441	12693	1	0.0E+00	AW887078.1	EST_HUMAN	MR1-SN0033-120400-002-004 SN0033 Homo sapiens cDNA
2335	7442	12694	6.53	0.0E+00	7682017	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2336	7443	12695	1.52	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2338	7443	12696	1.52	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2337	7444		2.39	0.0E+00	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
2339	7446	12698	19.43	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2339	7446	12699	19.43	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2339	7446	12700	19.43	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2340	7447	12701	1.59	0.0E+00	8923039	NT	Homo sapiens hypothetical protein FLJ20081 (FLJ20081), mRNA
2358	7455		4.27	0.0E+00	BE814424.1	EST_HUMAN	MR0-BN0070-090600-029-012 BN0070 Homo sapiens cDNA
2392	7498		3.25	0.0E+00	A042035.1	EST_HUMAN	alpha60b02.x1 Soares_NHIMPu_31 Homo sapiens cDNA clone IMAGE:1600683 3' similar to TR:008682
2394	7500	12761	4.39	0.0E+00	8923820	NT	O08682 230KDA PHOSPHATIDYLINOSITOL 4-KINASE. ;
2398	7502	12752	1	0.0E+00	AW303988.1	EST_HUMAN	bx1507.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2813221 3' similar to TR:064824
2398	7504		3.23	0.0E+00	BE895605.1	EST_HUMAN	601432608F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918168 5'
2410	7516		4.98	0.0E+00	AB005622.1	EST_HUMAN	AB005622 HeLa cDNA (T.Noma) Homo sapiens cDNA similar to adenylate kinase isozyme 2
2413	7519	12769	5.88	0.0E+00	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA

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2417	7522	12773	1.61	0.0E+00	D85606.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
2417	7522	12774	1.61	0.0E+00	D85606.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
2425	7530	12783	1.04	0.0E+00	AF106276.1	NT	Homo sapiens immunoglobulin-like transcript 10 variant 4 (ILT4) gene, exon 8
2429	7533	12788	1.5	0.0E+00	BF948274.1	EST_HUMAN	602018058F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4163870 5'
2436	7540	12794	2.44	0.0E+00	572877.1	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2439	7543	12798	1.13	0.0E+00	BE831003.1	EST_HUMAN	CMO-MT0033-150800-428-h11 MT0033 Homo sapiens cDNA
2439	7543	12797	1.13	0.0E+00	BE831003.1	EST_HUMAN	CMO-MT0033-150800-428-h11 MT0033 Homo sapiens cDNA
2444	7548	12801	37.91	0.0E+00	BF569144.1	EST_HUMAN	602184858T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300383 3'
2451	7555	12807	4.45	0.0E+00	AW468922.1	EST_HUMAN	hcd0404.x1 NCI_CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2872769 3'
2453	7557	12808	2.12	0.0E+00	AW501010.1	EST_HUMAN	UHF-BPOp-ab-c-07-o-U1.r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2476	7580		1.9	0.0E+00	AW813853.1	EST_HUMAN	RC3-ST0197-300300-018-c04 ST0197 Homo sapiens cDNA
2480	7585	12836	55.02	0.0E+00	BE795542.1	EST_HUMAN	601692830F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946518 5'
2481	7622	12868	1.18	0.0E+00	7857038	NT	Homo sapiens death receptor 6 (DR6), mRNA
2482	7586	12836	2.07	0.0E+00	BF509482.1	EST_HUMAN	UHF-BH-aaz-b-08-o-U1.a1 NCI_CGAP_Sub88 Homo sapiens cDNA clone IMAGE:3086556 3'
2485	7588	12838	1.28	0.0E+00	Z32684.2	NT	Homo sapiens mRNA for membrane transport protein (XK gene)
2487	7591		2.28	0.0E+00	6453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFRL) mRNA
2480	7594	12842	1.61	0.0E+00	BE910378.1	EST_HUMAN	601503356F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3905148 5'
2491	7595	12843	1.54	0.0E+00	7857488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2492	7598	12844	5.51	0.0E+00	BE150866.1	EST_HUMAN	RC4-HT0276-160200-013-405 HT0276 Homo sapiens cDNA
2493	7597	12845	3.17	0.0E+00	8923340	NT	Homo sapiens hypothetical protein FLJ20368 (FLJ20368), mRNA
2494	7598	12846	10.75	0.0E+00	U93239.1	NT	Human Sec62 (Sec62) mRNA, complete cds
2499	7603	12851	10.82	0.0E+00	BE888490.1	EST_HUMAN	601508211F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909868 5'
2504	7607	12857	3.04	0.0E+00	BE875511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2504	7607	12858	3.04	0.0E+00	BE875511.1	EST_HUMAN	601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2508	7608	12859	1.27	0.0E+00	AF114027.1	EST_HUMAN	AF114027 Homo sapiens lung fetus Homo sapiens cDNA clone ESF8
2507	7610	12862	1.44	0.0E+00	AF245505.1	NT	Homo sapiens ediclin mRNA, complete cds
2522	7628	12876	1.17	0.0E+00	BE536921.1	EST_HUMAN	601084738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5'
2528	7629	12876	11.25	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y78AA1 Homo sapiens cDNA clone Y78AA1001673 5'
2528	7628	12877	11.25	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y78AA1 Homo sapiens cDNA clone Y78AA1001673 5'
2527	7630	12878	1.85	0.0E+00	BE262898.1	EST_HUMAN	601105312F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2887955 5'
2527	7630	12878	1.85	0.0E+00	BE262898.1	EST_HUMAN	601105312F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2887955 5'
2530	7633	12881	4.83	0.0E+00	AF245505.1	NT	Homo sapiens ediclin mRNA, complete cds
2561	7878	12917	3.59	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2561	7878	12918	3.59	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2662	7663		1.77	0.0E+00	BF613836.1	EST_HUMAN	U1H-BW1-amp-f-12-0-UL.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'
2668	7669	12824	1.94	0.0E+00	BF672618.1	EST_HUMAN	602152653F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4283612 5'
2670	7671		1.23	0.0E+00	BE616695.1	EST_HUMAN	601278873F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3821788 5'
2676	7676	12830	4.12	0.0E+00	AB037742.1	NT	Homo sapiens mRNA for KIAA1321 protein, partial cds
2677	7677	12831	0.95	0.0E+00	AU571737.1	EST_HUMAN	h18608x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2168055 3' similar to gb128977 CALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE, BRAIN (ISOFORM 2 (HUMAN);
2678	7678	12832	2.82	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 28kD (TAF21) mRNA
2680	7681	12836	3.56	0.0E+00	AB037859.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
2681	7682	12837	1.35	0.0E+00	BE705446.1	EST_HUMAN	601580108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2681	7682	12838	1.35	0.0E+00	BE789446.1	EST_HUMAN	601580108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2691	7692		13.31	0.0E+00	BE792472.1	EST_HUMAN	601584630F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3839222 5'
2693	7694	12948	1.19	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
2693	7694	12955	3.59	0.0E+00	4504686	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
2692	7696	12959	0.99	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
2698	7707	12962	3.82	0.0E+00	AF173227.1	NT	Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1
2699	7710	12963	1.94	0.0E+00	AB011108.1	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
2699	7712	12965	1.12	0.0E+00	AU133385.1	EST_HUMAN	AU133385 NT2RP4 Homo sapiens cDNA clone NT2RP4001684 5'
2699	7713	12966	1.11	0.0E+00	M59225.1	NT	Human bullous pemphigoid antigen (BPAG1) mRNA, complete cds
2699	7715	12968	3.79	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2699	7715	12969	3.79	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2699	7716	12972	1.43	0.0E+00	AW887016.1	EST_HUMAN	RC1-OT0086-220300-011-407 OT0086 Homo sapiens cDNA
2699	7721	12973	1.95	0.0E+00	BF000018.1	EST_HUMAN	7h15h05x1 NCL CGAP_Co16 Homo sapiens cDNA clone IMAGE:3316089 3'
2699	7722	12976	4.51	0.0E+00	BE383165.1	EST_HUMAN	601288714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3828823 5'
2699	7723	12978	2.17	0.0E+00	BE531263.1	EST_HUMAN	601278373F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3810287 5'
2699	7747	12988	1.33	0.0E+00	8822843	NT	Homo sapiens hypothetical protein FLJ11052 (FLJ11052), mRNA
2699	7755	13006	1.25	0.0E+00	AB037732.1	NT	Homo sapiens mRNA for KIAA1311 protein, partial cds
2699	7761		24.89	0.0E+00	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L28
2699	7762	13030	43.93	0.0E+00	BE794894.1	EST_HUMAN	601588626F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943591 5'
2699	7767	13037	4.97	0.0E+00	U36263.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
2699	7768	13038	1.88	0.0E+00	7693517	NT	Homo sapiens neuregulin 1 (NRG1), transcript variant SMDF, mRNA
2699	7790	13040	1.55	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2699	7791	13041	2.6	0.0E+00	AB051826.1	NT	Homo sapiens H28K mRNA for GTP-binding protein like 1, complete cds

Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NC:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2700	7798	13047	90.08	0.0E+00	BE796376.1	EST_HUMAN	601581991F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945983 5'
2701	7797	13048	1.94	0.0E+00	BF680832.1	EST_HUMAN	602155923F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4287132 5'
2704	7949	13052	75.81	0.0E+00	BE663433.1	EST_HUMAN	601335485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689864 5'
2705	7800		2.71	0.0E+00	AV721847.1	EST_HUMAN	AV721847 HTB Homo sapiens cDNA clone HTBBYE09 5'
2707	7802	13055	1.9	0.0E+00	5174488	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2707	7802	13058	1.9	0.0E+00	5174488	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2708	7803	13057	1.94	0.0E+00	8823441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2708	7803	13058	1.94	0.0E+00	8823441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
2709	7804	13059	9.14	0.0E+00	AF260195.1	NT	Homo sapiens hypertensin-related calcium-regulated gene mRNA, complete cds
2710	7805		61.45	0.0E+00	AV651068.1	EST_HUMAN	AV651068 GLC Homo sapiens cDNA clone GLCCLD07 3'
2711	7806	13060	2.74	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-260900-439-508 TN0141 Homo sapiens cDNA
2711	7806	13061	2.74	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-260900-439-508 TN0141 Homo sapiens cDNA
2715	7810	13064	8.04	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2716	7810	13065	8.04	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2718	7814	13070	37.71	0.0E+00	BE747183.1	EST_HUMAN	601580803F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3828472 5'
2730	7825		1.28	0.0E+00	AL168201.2	NT	Homo sapiens chromosome 21 segment HS21O001
2731	7826	13081	2.6	0.0E+00	BF614110.1	EST_HUMAN	U1H-BW1-ermw-e-07-QUJ.st NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'
2742	7836	13089	1.66	0.0E+00	7705275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2742	7836	13090	1.66	0.0E+00	7705275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2743	7837	13091	2.45	0.0E+00	BF677694.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4246915 5'
2749	7843	13098	1.65	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPR), mRNA
2752	7846	13101	37.83	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTG Homo sapiens cDNA clone HTGCCA03 5'
2752	7846	13102	37.83	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTG Homo sapiens cDNA clone HTGCCA03 5'
2764	7848		14.98	0.0E+00	AU878183.1	EST_HUMAN	au85d04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518883 5' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
2757	7851	13107	2.14	0.0E+00	BF530681.1	EST_HUMAN	602071957F1 NCI_CGAP_Brm87 Homo sapiens cDNA clone IMAGE:4214878 5'
2768	7852	13108	147.71	0.0E+00	BE872788.1	EST_HUMAN	601450912F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854942 5'
2760	7854	13109	9.86	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002872 5'
2760	7854	13110	9.86	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002872 5'
2761	7855	13111	128.52	0.0E+00	BE300344.1	EST_HUMAN	60094784F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860808 5'
2761	7855	13112	128.52	0.0E+00	BE300344.1	EST_HUMAN	60094784F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860808 5'
2767	8376	10518	3.03	0.0E+00	S78830.1	NT	glycoprotein D-Duffy group antigen [human, blood, Genomic DNA, 3068 nt]
2770	7862		2.78	0.0E+00	AB033281.1	NT	Homo sapiens BTIRCP2 mRNA for F-box and WD-repeat protein isoform C, complete cds
2776	5888	11040	9.94	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds

Table 4

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2776	5888	11041	3.94	0.0E+00	AF264760.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2780	6182	11347	2.85	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (glucocorticoid-inducible), polypeptide 1 (glucocorticoid 3, primary infantile) (CYP1B1) mRNA
2780	6182	11348	2.85	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (glucocorticoid-inducible), polypeptide 1 (glucocorticoid 3, primary infantile) (CYP1B1) mRNA
2797	7854	13120	2.95	0.0E+00	X85980.1	NT	H. sapiens serine hydroxymethyltransferase pseudogene
2798	7856		1.43	0.0E+00	AF068624.1	NT	Homo sapiens 5-aminolevulinic acid synthase 2 (ALAS2) gene, complete cds
2800	7857		1.28	0.0E+00	AB040960.1	NT	Homo sapiens mRNA for KIAA1527 protein, partial cds
2807	7863		1.07	0.0E+00	AJ238852.1	NT	Homo sapiens partial rps3 gene for ribosomal protein L8, U82 snRNA, U83a snRNA and U83b snRNA genes
2808	7864	13125	2.44	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21O001
2812	7868	13128	5.27	0.0E+00	M80902.1	NT	Human AHNK nucleoprotein mRNA, 5' and
2816	7871	13130	1.01	0.0E+00	BE154504.1	EST_HUMAN	PMO-HT0343-281288-003-e02 HT0343 Homo sapiens cDNA
2816	7871	13131	1.01	0.0E+00	BE154504.1	EST_HUMAN	PMO-HT0343-281288-003-e02 HT0343 Homo sapiens cDNA
2817	7873		1.91	0.0E+00	X73428.1	NT	H. sapiens lds gene for HLH type transcription factor
2819	7875		2.62	0.0E+00	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21O068
2820	7876	13134	1.39	0.0E+00	7016584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2820	7876	13135	1.39	0.0E+00	7016584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2820	7876	13136	1.39	0.0E+00	7016584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2826	7881	13142	45.48	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2826	7881	13143	45.48	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2830	7886	13148	3.23	0.0E+00	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2831	7886		6.71	0.0E+00	Y10658.1	NT	H. sapiens mRNA for nuclear DNA helicase II
2832	7887		1.11	0.0E+00	AF152303.1	NT	Homo sapiens proboscidein alpha C1 (POSH-alpha-C1) mRNA, complete cds
2833	7888	13147	89.98	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2833	7888	13148	89.98	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2846	8001	13161	2.44	0.0E+00	4507280	NT	Homo sapiens serine/threonine kinase 9 (STK9) mRNA
2846	8004	13165	1.2	0.0E+00	AL047699.1	EST_HUMAN	DKFZp586G0621_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586G0621
2850	8005	13168	0.93	0.0E+00	7681883	NT	Homo sapiens KIAA0054 gene product: Helicase (KIAA0054), mRNA
2850	8005	13167	0.93	0.0E+00	7681883	NT	Homo sapiens KIAA0054 gene product: Helicase (KIAA0054), mRNA
2851	8006		1.55	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanocyte-associated) (CSPG4), mRNA
2854	8008	13169	5.69	0.0E+00	BE081898.1	EST_HUMAN	QV2-BT0636-130400-139-103 BT0636 Homo sapiens cDNA
2854	8009	13170	5.59	0.0E+00	BE081898.1	EST_HUMAN	QV2-BT0636-130400-139-103 BT0636 Homo sapiens cDNA
2859	8014	13178	0.82	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exam SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2859	8014	13178	0.82	0.0E+00	6805818	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2862	8017	13183	2	0.0E+00	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2862	8017	13184	2	0.0E+00	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2869	8023		9.71	0.0E+00	Y18210.1	NT	Homo sapiens HRB6 gene for hair keratin, exon 1 to 9
2872	8026	13183	1.05	0.0E+00	4768279	NT	Homo sapiens EphA4 (EPHA4) mRNA
2874	8028	13186	42.94	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2875	8029	13197	0.98	0.0E+00	AJ561002.1	EST_HUMAN	In18d07.x1 NC1_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247
2875	8029	13198	0.98	0.0E+00	AJ561002.1	EST_HUMAN	In18d07.x1 NC1_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167981 3' similar to TR:O16247
2876	8030	13189	1.47	0.0E+00	P52740	SWISSPROT	O16247 F4AE7.2 PROTEIN.; ZINC FINGER PROTEIN 132
2877	8031	13200	0.95	0.0E+00	AF15238.1	NT	Homo sapiens proteodherin gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2893	8047	13212	1.7	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
2893	8047	13213	1.7	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
2894	8048	13214	5.93	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1608 protein, partial cds
2894	8048	13215	5.93	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1608 protein, partial cds
2897	8051	13218	9.93	0.0E+00	7681903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2897	8051	13219	3.55	0.0E+00	7681903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2896	8052	13220	9.81	0.0E+00	6174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q23;q24) translocation), MLLT4 mRNA
2896	8052	13221	9.81	0.0E+00	6174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q23;q24) translocation), MLLT4 mRNA
2893	8058	13226	1.18	0.0E+00	BF110702.1	EST_HUMAN	7h4d03.x1 NC1_CGAP_LU24 Homo sapiens cDNA clone IMAGE:3587028 3' similar to TR:Q9VLN1
2893	8058	13226	1.18	0.0E+00	BF110702.1	EST_HUMAN	Q9VLN1 CG17293 PROTEIN.; 7h4d03.x1 NC1_CGAP_LU24 Homo sapiens cDNA clone IMAGE:3587028 3' similar to TR:Q9VLN1
2911	8065	13237	2.83	0.0E+00	4505094	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4) mRNA
2911	8065	13238	2.83	0.0E+00	4505094	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4) mRNA
2920	8074	13244	1.53	0.0E+00	4768827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
2921	8075		0.98	0.0E+00	X98494.1	NT	H. sapiens mRNA for M phase phosphoprotein 10
2924	8078	13247	1.5	0.0E+00	AB033094.1	NT	Homo sapiens mRNA for KIAA1208 protein, partial cds
2927	8081	13249	8.59	0.0E+00	AF106275.1	NT	Homo sapiens immunoglobulin-like transcript 1 variant 4 (LIT1c) gene, exon 6
2943	8097		0.98	0.0E+00	AI149880.1	EST_HUMAN	g43f09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1762809 3'
2943	8105	13270	2.42	0.0E+00	AA0004884.1	NT	Homo sapiens mRNA for PKU-alpha, partial cds

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2882	8116	13278	1.8	0.0E+00	7682273	NT	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA
2883	8117	13279	2.04	0.0E+00	5726755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2883	8117	13280	2.04	0.0E+00	6726755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2887	8121	13285	1.1	0.0E+00	AB037852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
2879	8128	13282	0.78	0.0E+00	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
2879	8128	13283	0.78	0.0E+00	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
2898	8183	13320	0.87	0.0E+00	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2898	8154	13313	1.15	0.0E+00	M74086.1	NT	Human displacement protein (CCAAT) mRNA
3009	8163	13320	0.85	0.0E+00	4506882	NT	Homo sapiens eemnogelin 1 (SEMG1) mRNA
3011	8165	13322	1.09	0.0E+00	AW076288.1	EST_HUMAN	EST388375 MAGE resequences, MAGN Homo sapiens cDNA
3016	8170	13322	3.92	0.0E+00	AF185953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
3019	8173	13330	6.89	0.0E+00	5579459	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3019	8173	13331	6.99	0.0E+00	5579459	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3021	8175	13331	6.28	0.0E+00	AL359403.1	NT	Isform 2 of a novel human mRNA from chromosome 22
3025	8178	13335	2.77	0.0E+00	AF017433.1	NT	Homo sapiens putative transcription factor CR63 (CR63) mRNA, partial cds
3028	8182		1.92	0.0E+00	AF198778.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM5 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
3048	8202	13358	3.16	0.0E+00	X03528.1	NT	Human germline gene 18.1 for Ig lambda L-chain C region (Ig-LC18.1)
3054	8207		1.54	0.0E+00	AF198355.1	NT	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds
3058	8211	13365	1.43	0.0E+00	AF084585.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
3082	8235	13385	4.28	0.0E+00	AF285208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3083	8236	13388	5.02	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3088	8241	13390	3.23	0.0E+00	7682139	NT	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA
3089	8242	13391	1.32	0.0E+00	AF042076.1	NT	Homo sapiens olfactory receptor-like protein (OLFR 428) gene, OLFR 428-9110 allele, partial cds
3119	8271	13427	3.27	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3129	8280	13438	50.99	0.0E+00	L20941.1	NT	Human ferritin heavy chain mRNA, complete cds
3132	8283	13439	1.16	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3132	8283	13440	1.16	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3139	8280	13447	22.17	0.0E+00	T94870.1	EST_HUMAN	ye32003.81 Striatogene lung (#837210) Homo sapiens cDNA clone IMAGE:119453 3' similar to SP-328539
3159	8306	13468	1.16	0.0E+00	BF243336.1	EST_HUMAN	S28539 BASIC PROTEIN, 23K -
3157	8308	13467	1.08	0.0E+00	AI968086.1	EST_HUMAN	801876507F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4107433 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3102	8313	13474	4.29	0.0E+00	X88822.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
3102	8313	13475	4.29	0.0E+00	X88822.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
3164	8316	13477	1.37	0.0E+00	AI685860.1	EST_HUMAN	tu38g08.X1 NCI_CQAP_P128 Homo sapiens cDNA clone IMAGE:2253376 3' similar to SW:RASD_DICD1
3176	8327	13480	1.73	0.0E+00	4758827	NT	P03967 RAS-LIKE PROTEIN RASD ;
3176	8327	13480	1.73	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NFXN3) mRNA
3183	8334	13497	8.16	0.0E+00	4504658	NT	Homo sapiens neuroxin III (NFXN3) mRNA
3202	8353	13515	6.29	0.0E+00	M26699.1	NT	Homo sapiens neuroxin III (NFXN3) mRNA
3206	8356	13517	2.69	0.0E+00	4502098	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
3211	8362	13525	0.79	0.0E+00	4758055	NT	(SLC25A5), nuclear gene encoding mitochondrial carrier, adenine nucleotide translocator, member 5
3211	8362	13525	0.79	0.0E+00	4758055	NT	Homo sapiens GREB binding protein (Rubinstein-Taybi syndrome) (GREBBP) mRNA
3213	8364	13527	34.87	0.0E+00	AA774783.1	EST_HUMAN	Homo sapiens GREB binding protein (Rubinstein-Taybi syndrome) (GREBBP) mRNA
3221	8372	13535	6.67	0.0E+00	AF286598.1	NT	ae87b11.e1 Stragene oct4a brain S11 Homo sapiens cDNA clone IMAGE:971133 3'
3221	8372	13536	6.67	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3231	8381	13541	1.18	0.0E+00	4567980	NT	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA
3236	8386	13548	0.92	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3244	8394	13558	1.1	0.0E+00	AF018413.1	NT	Homo sapiens HLA class III region containing transmembrane X (transmembrane-X) gene, partial cds; cytoblastome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helixase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes>
3247	8397	13559	4.03	0.0E+00	AF055084.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds
3250	8400	13561	1.25	0.0E+00	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
3250	8400	13562	1.25	0.0E+00	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
3258	10304	13569	2.51	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3258	10304	13570	2.51	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3274	8423	13584	3.1	0.0E+00	AF265208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3276	8424	13585	1.83	0.0E+00	8823824	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
3295	8442	13604	0.67	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
3305	8452	13614	4.47	0.0E+00	AI599294.1	EST_HUMAN	u6808.x2 NCI_CQAP_Par1 Homo sapiens cDNA clone IMAGE:222535 3' similar to SW:RL11_RAT
3313	8460	13622	2.76	0.0E+00	AF128893.1	NT	P25121 60S RIBOSOMAL PROTEIN L11, contains Alu repetitive element;
3313	8460	13623	2.76	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TER) gene, exons 1-8
3314	8461	13624	1.06	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3314	8461	13625	1.06	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3317	8484	13627	2.12	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3317	8484	13628	2.12	0.0E+00	4602582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3320	8487	13630	10.5	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MIEV) gene, complete cds
3322	8488	13632	1.78	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
3328	8476	13638	0.82	0.0E+00	BE779039.1	EST_HUMAN	601494898F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:38683248 5'
3338	8485	13651	0.74	0.0E+00	AI632589.1	EST_HUMAN	W610604.X1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2305279 3' similar to TR-O61928 Q61929
3377	8522	13688	6.85	0.0E+00	AU128684.1	EST_HUMAN	ZINC FINGER PROTEIN ;
3384	8528	13689	0.98	0.0E+00	7363438	NT	AU123684 NT2RM2 Homo sapiens cDNA clone NT2RM2000735 5'
3384	8528	13690	0.98	0.0E+00	7363438	NT	Homo sapiens difactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3387	8531	13692	1.88	0.0E+00	7706238	NT	Homo sapiens difactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3388	8532	13693	1.14	0.0E+00	AF211188.1	NT	Homo sapiens neuroblastoma-amplified protein (LOC31594), mRNA
3393	8537	13707	1.12	0.0E+00	AW867015.1	EST_HUMAN	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a isoform (CACNA1I) mRNA, complete cds
3408	8548	13707	1.44	0.0E+00	7682401	NT	MR1-SN0038-100400-001-c08 SN0033 Homo sapiens cDNA
3408	8548	13708	1.44	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3407	8550	13709	1.16	0.0E+00	4502398	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3409	8552	13710	1.95	0.0E+00	5803087	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA
3418	7780	13040	1.48	0.0E+00	AF110783.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3423	8565	13723	1.85	0.0E+00	7687038	NT	Homo sapiens death receptor 8 (DR8), mRNA
3426	8568	13727	1.19	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
3428	8568	13728	1.19	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
3427	8568	13728	4.88	0.0E+00	K02380.1	NT	Bacteriophage P1 replication region including repA, parA, and parB genes and IncA, IncB, and IncC
3428	8571	13731	1.17	0.0E+00	7427622	NT	Incompatibility determinants
3437	8578	13738	4.18	0.0E+00	AI835159.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
3437	8578	13739	4.18	0.0E+00	AI835159.1	EST_HUMAN	WP14610.X1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR-O73834 O73834
3441	8583	13744	2.5	0.0E+00	AJ278120.1	NT	NEURAL CELL ADHESION MOLECULE ;
3447	8588	13752	4.5	0.0E+00	6552332	NT	WP14610.X1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR-O73834 O73834
3447	8588	13763	4.5	0.0E+00	6552332	NT	NEURAL CELL ADHESION MOLECULE ;
3453	8595	13769	1.7	0.0E+00	M14123.1	NT	Homo sapiens mRNA for putative enkyrin-repeat containing protein (ORF1)
							Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
							Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
							Human endogenous retrovirus HERV-K10

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3458	8600	13784	5.97	0.0E+00	U43293.1	NT	Human MDS1A (AML1/MDS1 fusion) mRNA, partial cds
3463	8605	13788	0.96	0.0E+00	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3463	8606	13789	0.96	0.0E+00	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3467	8609	13774	2.46	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3467	8609	13775	2.46	0.0E+00	AF045452.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3474	8616	13783	0.97	0.0E+00	AF231922.1	NT	Homo sapiens chromosome 21 unknown mRNA
3479	8620	13785	1.12	0.0E+00	AJ010770.1	NT	Homo sapiens hypoxanthine gene, exons 1-50
3481	8622	13787	1.1	0.0E+00	AA626877.1	EST_HUMAN	ab51112.1 Strabagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:844387 5'
3481	8622	13788	1.1	0.0E+00	AA626877.1	EST_HUMAN	ab51112.1 Strabagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:844387 5'
3481	8622	13789	1.1	0.0E+00	AA626877.1	EST_HUMAN	ab51112.1 Strabagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:844387 5'
3485	8626	13793	1.02	0.0E+00	4508028	NT	Homo sapiens zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide) (ZNF45) mRNA
3488	8629	13795	2.4	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3488	8629	13796	2.4	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3492	8633	13800	0.89	0.0E+00	4826798	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNK2) mRNA
3495	8636	13803	1.92	0.0E+00	C14897	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HAZ303)
3499	8640	13808	0.82	0.0E+00	AJ384007.1	EST_HUMAN	bc36g12.x1 Soares_NhlhMPu_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:000498
3502	8643	13809	1.26	0.0E+00	M10976.1	NT	Q00488 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN ; Human endogenous retroviral DNA (4-1), complete retroviral segment
3519	8650	13827	0.77	0.0E+00	AB032979.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds
3519	8650	13828	0.77	0.0E+00	AB032979.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds
3526	8658	13834	1.13	0.0E+00	AB029019.1	NT	Homo sapiens mRNA for KIAA1096 protein, partial cds
3526	8670	13835	1.29	0.0E+00	AV701869.1	EST_HUMAN	AV701869 ADB Homo sapiens cDNA clone ADBDAH08 5'
3529	8671	13836	0.87	0.0E+00	4808884	NT	Homo sapiens semenogelin II (SEM2) mRNA
3531	8673	13844	2.24	0.0E+00	AF078988.1	NT	Homo sapiens homologous yeast-44.2 protein mRNA, complete cds
3539	8681	13844	0.96	0.0E+00	AL133204.1	NT	Novel human gene mapping to chromosome X
3541	8682	13845	1.16	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1478 protein, partial cds
3551	8692	13854	2.09	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
3561	8702	13862	1.08	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3561	8702	13863	1.09	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3562	8703		1.39	0.0E+00	AI081907.1	EST_HUMAN	cc77c11.x1 Soares_NhlhMPu_S1 Homo sapiens cDNA clone IMAGE:1662358 3' similar to WP:11984.4 CE13742 ;
3564	8705	13866	1.09	0.0E+00	6325493	NT	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA
3569	8710		4.53	0.0E+00	AW852217.1	EST_HUMAN	QV6-CT0226-230300-169-ed1 CT0226 Homo sapiens cDNA

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3576	8717		0.92	0.0E+00	AF118848.1	NT	Homo sapiens gamma-glutamylcysteine synthetase (GLCLC) gene, partial cds
3577	8718	13875	6.8	0.0E+00	BF676393.1	EST_HUMAN	602084593F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248598 5'
3588	8728	13885	1.05	0.0E+00	AW693797.1	EST_HUMAN	QVQ-DT0047-17020-123-g01 DT0047 Homo sapiens cDNA
3593	8737	13890	1.23	0.0E+00	BF672054.1	EST_HUMAN	602162488F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4233845 6'
3598	8737	13891	1.23	0.0E+00	BF672054.1	EST_HUMAN	602162488F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4233845 6'
3599	8738		1.31	0.0E+00	4826967	NT	Homo sapiens retinol-binding protein 2 (RBP2) mRNA
3601	8740	13893	0.72	0.0E+00	AW684683.1	EST_HUMAN	hB4g01.x1 Soares_NFL_T_GBC_31 Homo sapiens cDNA clone IMAGE:2878024 3'
3601	8740	13894	0.72	0.0E+00	AW684683.1	EST_HUMAN	hB4g01.x1 Soares_NFL_T_GBC_31 Homo sapiens cDNA clone IMAGE:2878024 3'
3603	8742	13896	0.71	0.0E+00	4826973	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1) mRNA
3605	8744	13899	1.06	0.0E+00	7682319	NT	Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
3610	8749	13905	1.19	0.0E+00	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3610	8749	13906	1.19	0.0E+00	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
3625	8764	13918	2.89	0.0E+00	D87327.1	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds
3628	8767		39.83	0.0E+00	7689491	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
3644	8783	13937	4.72	0.0E+00	AB026642.1	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
3646	8785	13939	1.12	0.0E+00	AB007668.2	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3648	8787	13940	4.08	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3648	8787	13941	4.08	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3657	8788	13951	1.59	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3657	8789	13952	1.59	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3660	8789	13955	1.22	0.0E+00	AW851714.1	EST_HUMAN	MR2-CT0222-281089-005-e05 CT0222 Homo sapiens cDNA
3664	8801	13957	2.19	0.0E+00	5729928	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3664	8803	13959	1.06	0.0E+00	AB018339.1	NT	Homo sapiens mRNA for KIAA0786 protein, partial cds
3666	8805	13961	1.62	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2803)
3668	8807	13963	1.16	0.0E+00	7682237	NT	Homo sapiens KIAA0870 protein/acidus (KIAA0870), mRNA
3668	8807	13964	1.15	0.0E+00	7682237	NT	Homo sapiens KIAA0870 protein/acidus (KIAA0870), mRNA
3682	8821	13976	4.6	0.0E+00	AW298134.1	EST_HUMAN	UHHBWO-dis-e-12-Q-U1.at NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2733022 3'
3682	8821	13977	4.6	0.0E+00	AW298134.1	EST_HUMAN	UHHBWO-dis-e-12-Q-U1.at NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2733022 3'
3710	8848	14002	1	0.0E+00	AB004630.1	NT	Human gene for Type XX collagen at chain, exon 8
3711	8849	14003	0.9	0.0E+00	AA463669.1	EST_HUMAN	aa08601.r1 Soares_NHIMPJ_S1 Homo sapiens cDNA clone IMAGE:812488 5' similar to SW_KBR4_SHEEP_P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIB4, [1];
3718	8854	14008	1.5	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0803 protein, partial cds
3719	8857	14010	3.8	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3728	8865	14019	0.92	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3740	8878	14029	5.49	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3743	8881	14032	35.82	0.0E+00	4508718	NT	Homo sapiens ribosomal protein S2 (RPS2), mRNA
3751	8888	14038	1.22	0.0E+00	7687065	NT	Homo sapiens v-src avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3761	8893	14039	1.22	0.0E+00	7687063	NT	Homo sapiens v-src avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3768	8935		0.95	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
3789	8936	14082	2.6	0.0E+00	AF178733.1	NT	Human trophoblasts olfactory receptor (PTR208) gene, partial cds
3802	8939	14086	2.11	0.0E+00	7657483	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3802	8939	14087	2.11	0.0E+00	7657488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3803	8940	14088	1.31	0.0E+00	AF020091.1	NT	Homo sapiens smooth muscle myosin heavy chain SM1 mRNA, alternatively spliced, partial cds
3807	8944	14083	1.23	0.0E+00	4759011	NT	Homo sapiens RAB9, member RAS oncogene family (RAB9) mRNA
3810	8947		1.29	0.0E+00	AF152496.1	NT	Homo sapiens protocadherin beta 3 (POGH-beta3) mRNA, complete cds
3811	8948	14098	3.81	0.0E+00	4758189	NT	Homo sapiens desmoglein (DPI, DP1) (DSP) mRNA
3814	8951	14099	20.71	0.0E+00	S76985.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6) mRNA
3816	8953	14101	2.23	0.0E+00	7710148	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA
3817	8954	14102	0.95	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3820	8957	14104	0.95	0.0E+00	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3820	8957	14105	0.95	0.0E+00	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3825	8961	14110	0.93	0.0E+00	AB001623.1	NT	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
3825	8961	14111	0.93	0.0E+00	AB001623.1	NT	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
3828	8964	14115	0.7	0.0E+00	6812735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
3833	8969	14123	6.36	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
3833	8969	14124	6.36	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 8 (CXORF8) mRNA
3835	8971	14127	4.16	0.0E+00	U09412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3836	8972	14128	0.87	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3839	8975	14130	1.24	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3842	8978	14133	0.91	0.0E+00	AF012615.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
3843	8979	14134	2.52	0.0E+00	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP128), mRNA
3945	8981	14136	0.6	0.0E+00	AF099117.1	NT	Homo sapiens amphipathin gene, partial cds
3953	8989	14145	2.76	0.0E+00	AI884727.1	EST_HUMAN	wk0101.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411055 3' similar to TRC043340
3956	8992	14149	13.45	0.0E+00	4508742	NT	O49340 R28830.2 : contains element PTR7 repetitive element;
3960	8996	14153	1.84	0.0E+00	AL040338.1	EST_HUMAN	Homo sapiens ribosomal protein S8 (RPS8) mRNA
							DKFZp434N0413_r1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434N0413 5'

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3894	9000	14167	2.4	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP-1), mRNA
3884	9000	14168	2.4	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP-1), mRNA
3888	9002	14160	2.09	0.0E+00	4504138	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA
3888	9004		1.7	0.0E+00	4505078	NT	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA
3872	9008	14184	1.22	0.0E+00	AF1494.1	NT	Homo sapiens HBP17 hepatit-binding and FGF-binding protein gene, complete cds
3881	9017	14174	1.66	0.0E+00	4308768	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
3885	9021	14178	2.16	0.0E+00	4585942	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
3890	9026	14184	3.22	0.0E+00	BF355285.1	EST_HUMAN	RC3-HIT0860-1/0800-011-e12 HIT0860 Homo sapiens cDNA
3881	9027	14185	2.82	0.0E+00	AW888221.1	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1986728 similar to MXRA5
3881	9027	14186	2.02	0.0E+00	AW888221.1	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1986728 similar to MXRA5
3890	9035	14194	1.68	0.0E+00	AF128583.1	NT	Homo sapiens F-box protein Fbl38 (FBL38) mRNA, partial cds
3902	9038	14197	0.83	0.0E+00	U86281.1	NT	Homo sapiens ciliary receptor (OR7-141) gene, partial cds
3902	9038	14198	0.93	0.0E+00	U86281.1	NT	Homo sapiens ciliary receptor (OR7-141) gene, partial cds
3905	9041	14201	3.91	0.0E+00	BCE378602.1	EST_HUMAN	PM3-LT0031-100100-003-H09 LT0031 Homo sapiens cDNA
3913	9049	14208	1.33	0.0E+00	AW680740.1	EST_HUMAN	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3948	9083	14235	4.18	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3948	9083	14236	4.18	0.0E+00	AF116195.1	NT	Human MHC class II lymphocyte antigen DPw4-beta-2 pseudogene, exon 2
3959	9094		3.95	0.0E+00	M23010.1	NT	Homo sapiens chromosome 21 segment HS21C0103
3962	9097		5.73	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C0184
3972	9106	14254	2.97	0.0E+00	AL163384.2	NT	Homo sapiens chromosome 21 segment HS21C0388
3980	9114	14282	2.12	0.0E+00	AL163386.2	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
3993	9127		79.42	0.0E+00	4503470	NT	HS5G08.X1 NCJ CGAP_G08 Homo sapiens cDNA clone IMAGE:2244734.3 similar to TR-O60308 O60309
3987	9131		1.29	0.0E+00	AI657078.1	EST_HUMAN	KIAA0563 PROTEIN ;
4000	9133	14277	2.32	0.0E+00	U06365.1	NT	Human zinc finger protein ZNF133
4020	9152	14296	6.2	0.0E+00	AB016610.1	NT	Chlorococcus ethiops mRNA for ribosomal protein S4X, complete cds
4028	9160		3.39	0.0E+00	AJ238817.1	NT	Homo sapiens mRNA for UGA suppressor RNA-associated antigenic protein (RNA48 gene)
4041	9172	14313	2.42	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C0003
4042	9173	14314	2.68	0.0E+00	AJ272728.1	NT	Homo sapiens mRNA for rape-2 (rape gene)
4042	9173	14315	2.68	0.0E+00	AJ272728.1	NT	Homo sapiens mRNA for rape-2 (rape gene)
4048	9180	14321	7.15	0.0E+00	5032028	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4048	9180	14322	7.15	0.0E+00	5032028	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA

Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4061	9192	14333	0.87	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycylamide formyltransferase, phosphoribosylglycylamide synthetase, phosphoribosylaminimidazole synthetase (GART) mRNA
4068	9196	14335	4.93	0.0E+00	4885308	NT	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA
4087	9197	14338	1.34	0.0E+00	AB006826.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
4070	9200	14337	7.7	0.0E+00	11418297	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA
4071	9201	14338	4.26	0.0E+00	AL094857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4078	9208	14346	3.09	0.0E+00	AF165627.1	NT	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds
4087	9270	11433	1.8	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4087	9270	11434	1.8	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4091	9220	14356	1.34	0.0E+00	4503864	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4091	9220	14357	1.34	0.0E+00	4503864	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
4094	9223	14359	1.34	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4094	9223	14360	1.34	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4098	9227	14363	0.9	0.0E+00	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
4104	9233	14370	4.5	0.0E+00	AI882637.1	EST_HUMAN	wu04d04.x1 NCL CGAP GC8 Homo sapiens cDNA clone IMAGE:2515978 3'
4104	9233	14371	4.5	0.0E+00	AI882637.1	EST_HUMAN	wu04d04.x1 NCL CGAP GC8 Homo sapiens cDNA clone IMAGE:2515978 3'
4107	9236	14373	1.33	0.0E+00	BE184858.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4107	9236	14374	1.33	0.0E+00	BE184858.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4112	9240	14374	3.98	0.0E+00	BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867680 5'
4117	9245	14381	4.44	0.0E+00	AB032951.1	NT	Homo sapiens mRNA for KIAA1125 protein, partial cds
4117	9245	14382	4.44	0.0E+00	AB032951.1	NT	Homo sapiens mRNA for KIAA1125 protein, partial cds
4119	9247	14384	0.92	0.0E+00	4507478	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
4120	9248	14385	3.12	0.0E+00	5728725	NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA
4128	9288		6.44	0.0E+00	AW676599.1	EST_HUMAN	ba51f04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900085 3' similar to SW:TH2_BOVIN
4133	9291	14399	1.02	0.0E+00	AW408788.1	EST_HUMAN	Q96108 MITOCHONDRIAL THOREDOXIN PRECURSOR ;
4134	9292	14400	1.94	0.0E+00	8922468	NT	UHF-BMD-adv-c-02-0-UL1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3083147 5'
4134	9292	14401	1.94	0.0E+00	8922468	NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4143	9271		2.37	0.0E+00	6174632	NT	Homo sapiens polycystic kidney diseases (polycystin) and REJ (sperm receptor for egg jelly, oca utrohin homolog)-like (PKDREJ) mRNA
4155	9281	14417	0.99	0.0E+00	AB037739.1	NT	Homo sapiens mRNA for KIAA1318 protein, partial cds
4163	9289	14424	9.44	0.0E+00	AA401438.1	EST_HUMAN	zu68h07.s1 Soares_test8_NHT Homo sapiens cDNA clone IMAGE:743187 3' similar to cortaine Alu repetitive element; contains element MER35 repetitive element ;

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4163	9289	14425	9.44	0.0E+00	AA401438.1	EST_HUMAN	z168107.s1 Soares_basilia_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element/contains element MER35 repetitive element;
4167	9293	14431	1.18	0.0E+00	AF157478.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
4181	9307	14444	1.22	0.0E+00	7682123	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
4183	5216	10328	1.12	0.0E+00	AA228128.1	EST_HUMAN	z158d04.L1 Soares_NH-IMPu_S1 Homo sapiens cDNA clone IMAGE:687560 5' similar to TR:G222811
4183	5216	10329	1.12	0.0E+00	AA228128.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN.;
4188	9321	14463	1.21	0.0E+00	7681869	NT	z158d04.L1 Soares_NH-IMPu_S1 Homo sapiens cDNA clone IMAGE:687560 5' similar to TR:G222811
4189	9324	14464	13.69	0.0E+00	4758199	NT	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN.;
4189	9324	14465	13.69	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4208	9333	14490	0.85	0.0E+00	AL163303.2	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4233	9358	14490	1.07	0.0E+00	AJ010770.1	NT	Homo sapiens chromosome 21 segment HS21C103
4247	9372	14505	4.01	0.0E+00	J02810.1	NT	Homo sapiens hypoxanthine gene, exons 1-50
4262	9387	14524	1.06	0.0E+00	AW596889.1	EST_HUMAN	Human apolipoprotein B-100 mRNA, complete cds
4287	9475	13638	0.6	0.0E+00	BE779039.1	EST_HUMAN	PM2-DT0023-080300-004-s08 DT0023 Homo sapiens cDNA
4271	9395	14534	4.79	0.0E+00	AF174590.1	NT	601484989F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3868246 5'
4279	9402	14541	0.64	0.0E+00	6803918	NT	Homo sapiens F-box protein Fbx4 (FBL4) mRNA, partial cds
4279	9402	14542	0.64	0.0E+00	6803918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4280	9403		2.49	0.0E+00	AI189844.1	EST_HUMAN	q223106.L1 Soares_Piacenta_8b39weeks_2NHb-IPb09W Homo sapiens cDNA clone IMAGE:1724579 3'
4284	9406		4.17	0.0E+00	U14520.1	NT	similar to contains MER20 b2 MER20 repetitive element;
4287	9409	14545	1.04	0.0E+00	5174674	NT	Human CBFA3 (Cbfa3) gene, partial cds
4288	9418	14551	0.81	0.0E+00	4505846	NT	Homo sapiens myeloid lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
4302	9424	14558	1.01	0.0E+00	6863384	NT	Homo sapiens propionin convertase subtilisin/kexin type 2 (PCSK2) mRNA
4302	9424	14559	1.01	0.0E+00	6863384	NT	Homo sapiens protein Kinase C, nu (PRKCN), mRNA
4308	9430	14566	1.11	0.0E+00	U10891.1	NT	Homo sapiens protein Kinase C, nu (PRKCN), mRNA
4308	9430	14568	1.11	0.0E+00	U10891.1	NT	Human G2 protein mRNA, partial cds
4318	9440	14573	8.66	0.0E+00	6912281	NT	Human G2 protein mRNA, partial cds
4333	9460		1.1	0.0E+00	AF153047.2	NT	Homo sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR), mRNA
4343	9465	14601	1.31	0.0E+00	U03601.1	NT	Homo sapiens gap junction protein connexin-36 (CX36) gene, complete cds
4349	9471	14608	4.62	0.0E+00	L14581.1	NT	Human Ig light chain VL1 region germline (humVL1c2c) gene, partial cds
							Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds

Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4353	9475	14613	4.82	0.0E+00	Z80780.1	NT	H.sapiens H2B/h gene
4353	9475	14614	4.82	0.0E+00	Z80780.1	NT	H.sapiens H2B/h gene
4354	9476	14615	1.17	0.0E+00	AW166833.1	EST_HUMAN	Xg68e10.X1 NCI_CGAP U14 Homo sapiens cDNA clone IMAGE:2833514 3' similar to TRP-07386 P07386
4360	9482	14621	1.55	0.0E+00	X60483.1	NT	ZINC FINGER PROTEIN 84;
4360	9482	14622	1.55	0.0E+00	X60483.1	NT	H.sapiens H4/d gene for H4 histone
4366	9486	14628	8.91	0.0E+00	7682091	NT	H.sapiens H4/d gene for H4 histone
4366	9486	14629	8.91	0.0E+00	7682091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4373	9494	14638	1.28	0.0E+00	X82338.1	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4376	9497	14642	15.1	0.0E+00	4886128	NT	Homo sapiens Marfan disease gene, exon 4
4377	9498	14643	1.48	0.0E+00	AJ271736.1	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4378	9499	14645	0.88	0.0E+00	AL163207.2	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4381	9502	14645	1.08	0.0E+00	AB037781.1	NT	Homo sapiens chromosome 21 segment HS21C007
4410	9530	14670	1.24	0.0E+00	7019458	NT	Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA
4420	9540	14670	0.81	0.0E+00	AF186963.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNP/EP2) gene, complete cds
4426	9548	14684	2.27	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4426	9548	14685	2.27	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4430	9549	14691	0.75	0.0E+00	W28178.1	EST_HUMAN	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4430	9549	14692	0.76	0.0E+00	W28178.1	EST_HUMAN	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4447	9588		2.08	0.0E+00	AF200829.1	NT	Homo sapiens HPS1 gene, Intron 5
4487	9596		1	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
4478	9598	14737	31.08	0.0E+00	AW084884.1	EST_HUMAN	Xc68e08.X1 NCI_CGAP Eso2 Homo sapiens cDNA clone IMAGE:2689448 3' similar to SW:AHNK_HUMAN
4480	10310		1.72	0.0E+00	8051619	NT	Q09688 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK ;
4482	9601	14740	0.81	0.0E+00	AF016050.1	NT	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA
4484	9603	14749	8.23	0.0E+00	AL163207.2	NT	Homo sapiens vascular endothelial cell growth factor 165 receptor/neuropilin (VEGF165) mRNA, complete cds
4491	9610	14749	1.27	0.0E+00	AJ278120.1	NT	Homo sapiens chromosome 21 segment HS21C007
4491	9610	14760	1.27	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4493	9612	14762	1.18	0.0E+00	4769487	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4494	9613	14763	2.95	0.0E+00	AF108830.1	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4498	9618	14769	1.01	0.0E+00	4508952	NT	Homo sapiens serine-threonine protein kinase (MNBI) mRNA, complete cds
4504	9623	14795	1.14	0.0E+00	S78684.1	NT	Homo sapiens sialyltransferase 8 (alpha-N-acetylneuraminic acid alpha-2,8-sialyltransferase, GD3 synthase) (SIAT8) mRNA
						NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, exon

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Table 4

Single Exon Probes Expressed In BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4506	9824	14768	1.38	0.0E+00	AF111183.1	NT	Homo sapiens pyrin (MEPV) gene, complete cds
4506	9824	14767	1.38	0.0E+00	AF111183.1	NT	Homo sapiens pyrin (MEPV) gene, complete cds
4512	10311	14776	2.71	0.0E+00	6008973	NT	Homo sapiens zinc finger protein 195 (ZNF195), mRNA
4517	9835	14780	5.93	0.0E+00	AF208161.1	NT	Homo sapiens synovial precursor, mRNA, complete cds
4522	9840	14787	1.15	0.0E+00	AF152337.1	NT	Homo sapiens protocadherin gamma C3 (PODH-gamma-C3) mRNA, complete cds
4526	9843	14791	1.98	0.0E+00	6464175	NT	Homo sapiens zinc finger protein 211 (ZNF211), mRNA
4536	9854	14799	44.34	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4543	9861	14804	0.87	0.0E+00	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 8 (LRP8) mRNA, and translated products
4547	9866	14807	1.06	0.0E+00	4503088	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (necanoma-associated) (CSPG4), mRNA
4552	9870	14813	1.48	0.0E+00	4502598	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA
4555	9873		1.52	0.0E+00	BE871908.1	EST_HUMAN	601447832F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3852127 5'
4558	9876		2.82	0.0E+00	L35485.1	NT	Homo sapiens adenosine triphosphatase (IDS) gene, complete cds
4560	9878	14816	10.88	0.0E+00	7682091	NT	Homo sapiens KIAA0380 gene product (KIAA0380), mRNA
4560	9878	14817	10.88	0.0E+00	7682091	NT	Homo sapiens KIAA0380 gene product (KIAA0380), mRNA
4575	9883	14830	2.49	0.0E+00	AF143314.1	NT	Homo sapiens PTEN (PTEN) gene, exons 3 through 5
4578	9888						Homo sapiens mRNA for G7o protein (G7o gene located in the class III region of the major histocompatibility complex)
4578	9888	14833	10.97	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7o protein (G7o gene located in the class III region of the major histocompatibility complex)
4578	9888	14834	10.97	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7o protein (G7o gene located in the class III region of the major histocompatibility complex)
4593	9711		2.31	0.0E+00	AA174072.1	EST_HUMAN	zot18g08.s1 Strabagene fetal retina B37202 Homo sapiens cDNA clone IMAGE:608854 3'
4595	9713		1.47	0.0E+00	7657410	NT	Homo sapiens cdc (odd Oz/ter-m, Drosophila) homolog 1 (ODZ1), mRNA
4597	9716		2.4	0.0E+00	AL163284.2	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4598	9716	14862	1.39	0.0E+00	AF184110.1	NT	Homo sapiens chromosome 21 segment HS21C100
4598	9717	14853	4.87	0.0E+00	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4600	9718		1.71	0.0E+00	AB037621.1	NT	Homo sapiens gene for nafuretic protein, partial cds
4602	9720	14854	0.74	0.0E+00	AF195656.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
4606	9724	14859	0.98	0.0E+00	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4608	9727	14863	1.09	0.0E+00	AL162331.1	NT	Novel human gene mapping to chromosome 1
4611	9728	14865	30.74	0.0E+00	4567887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4611	9728	14868	30.74	0.0E+00	4567887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4612	9730	14867	2.55	0.0E+00	AF157441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
4621	9738	14878	0.81	0.0E+00	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4621	9738	14879	0.81	0.0E+00	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4621	9739	14880	0.91	0.0E+00	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4622	9740	14881	1.18	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4623	9741	14882	1.18	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4624	9742	14883	10.76	0.0E+00	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
4625	9743	14884	1.28	0.0E+00	BE081927.1	EST_HUMAN	QV2-BT0635-169400-142-105 BT0635 Homo sapiens cDNA
4626	9744	14885	1.42	0.0E+00	AA418246.1	EST_HUMAN	z08b07.s1 Soares_NIHMPU_S1 Homo sapiens cDNA clone IMAGE767605 3'
4627	9745	14886	2.12	0.0E+00	AF088841.1	NT	Homo sapiens truncated tensin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region
4628	9746	14887	2.23	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1389 protein, partial cds
4629	9747	14888	2.23	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1389 protein, partial cds
4630	9748	14889	2.34	0.0E+00	M74089.1	NT	Human displacement protein (CQAA1) mRNA
4631	9749	14890	1.02	0.0E+00	AW294800.1	EST_HUMAN	UHH-B12-shi-c-05-Q-U1.s1 NCL CGAP_Sub4 Homo sapiens cDNA clone IMAGE2728782 3'
4632	9750	14891	1.02	0.0E+00	AW294800.1	EST_HUMAN	UHH-B12-shi-c-05-Q-U1.s1 NCL CGAP_Sub4 Homo sapiens cDNA clone IMAGE2728782 3'
4633	9751	14892	2.18	0.0E+00	8453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4634	9752	14893	2.18	0.0E+00	8453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4635	9753	14894	4.19	0.0E+00	T66945.1	EST_HUMAN	y683g04.12 Strategene fetal spleen (#637205) Homo sapiens cDNA clone IMAGE-88310 5'
4636	9754	14895	4.19	0.0E+00	T66945.1	EST_HUMAN	y683g04.12 Strategene fetal spleen (#637205) Homo sapiens cDNA clone IMAGE-88310 5'
4637	9755	14896	44.66	0.0E+00	M80902.1	NT	Human AHNK nucleoporin mRNA, 5' end
4638	9756	14897	1.81	0.0E+00	M89197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4639	9757	14898	1.91	0.0E+00	M89197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4640	9758	14899	1.82	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTTR) gene, complete cds
4641	9759	14900	0.73	0.0E+00	7662479	NT	Homo sapiens KIAA1084 protein (KIAA1084), mRNA
4642	9760	14901	2.63	0.0E+00	7662181	NT	Homo sapiens KIAA0563 gene product (KIAA0563), mRNA
4643	9761	14902	1.86	0.0E+00	U07563.1	NT	Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds
4644	9762	14903	1.18	0.0E+00	AL095857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4645	9763	14904	1.28	0.0E+00	X58487.1	NT	Human CYP2D7AP pseudogene for cytochrome P450 2D6
4646	9764	14905	1.09	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4647	9765	14906	1.09	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4648	9766	14907	1.27	0.0E+00	AF028901.1	NT	Homo sapiens alpha-3 type IX collagen (COL3A3) gene, promoter region, and exons 1-28
4649	9767	14908	1.04	0.0E+00	6877700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4650	9768	14909	1.04	0.0E+00	6877700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4651	9769	14910	0.83	0.0E+00	7018320	NT	Homo sapiens protein0008 (AD013), mRNA
4652	9770	14911	0.83	0.0E+00	7018320	NT	Homo sapiens protein0008 (AD013), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4753	9888	15015	1.74	0.0E+00	AW444837.1	EST_HUMAN	U1H-B13-qlw-c-04-U1.s1 NC1 CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2733294 3'
4759	9872	15023	1.41	0.0E+00	AF303134.1	NT	Homo sapiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds
4762	9876		1.63	0.0E+00	AF083242.1	NT	Homo sapiens HSPC024-Iso mRNA, complete cds
4807	9818	15060	1.09	0.0E+00	5901853	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
4810	9922						Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4814	9928	15087	4.79	0.0E+00	AF240786.1	NT	Mfascicularis mRNA for metalloproteinase-like, disintegrin-like protein, IVa
4816	9928	15069	3.26	0.0E+00	X87205.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCH9) mRNA, complete cds
4818	9930	15071	2.79	0.0E+00	AF084479.1	NT	Mus musculus zinc finger transcription factor Kalso mRNA, complete cds
4819	9931	15072	2.11	0.0E+00	AF097416.1	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4821	9933	15074	4.47	0.0E+00	4603768	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA
4822	9934	15076	27.4	0.0E+00	4885048	NT	ZINC FINGER PROTEIN 132
4824	9938	15077	1.43	0.0E+00	P82740	SWISSPROT	Homo sapiens hypothetical protein DKFp762E1312 (DKFp762E1312), mRNA
4827	9939	15081	1.33	0.0E+00	8922180	NT	Homo sapiens hypothetical protein FLJ20073 (FLJ20073), mRNA
4831	9943	15085	8.77	0.0E+00	8923080	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4832	9944	15086	1.25	0.0E+00	7691978	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4832	9944	15087	1.61	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4834	9948	15089	1.61	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1-J61 segments; and Tcr-C-alpha gene, exons 1-4
4834	9946	15080	1.15	0.0E+00	X94628.1	NT	H. sapiens MeCP-2 gene
4838	9950	15094	1.15	0.0E+00	X94628.1	NT	H. sapiens MeCP-2 gene
4840	9952	15097	2.24	0.0E+00	AL165280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4840	9952	15097	1.05	0.0E+00	7708604	NT	Homo sapiens MAGC-C2 (MAGC2), mRNA
4848	9960	15104	1.05	0.0E+00			Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, I, 28kD (TAF2i) mRNA
4854	9968	15111	1.26	0.0E+00	5032150	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4856	9968	15113	0.8	0.0E+00	6806918	NT	Homo sapiens MICA gene
4858	9970	15119	1.3	0.0E+00	X92841.1	NT	H. sapiens MICA gene
4859	9971	15116	2.22	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIAA0412) mRNA
4860	9972	15117	1.28	0.0E+00	AB037864.1	NT	Homo sapiens mRNA for KIAA1443 protein, partial cds
4861	9973	15118	0.9	0.0E+00	Y06232.1	NT	H. sapiens ferritin alpha pseudogene
4862	9974	15119	2.01	0.0E+00	AB014633.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
4863	9975	15120	2.39	0.0E+00	6977848	NT	Mus musculus zinc finger protein interacting with K protein 1 (Zik1), mRNA
4864	9976	15121	1.5	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 8 (colloid-cd1 prolidase-1) (MGEA8), mRNA
4864	9976	15121	2.18	0.0E+00	BE007835.1	EST_HUMAN	QV0-BN0147-280400-213-q11 BN0147 Homo sapiens cDNA

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Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4884	9876	15122	2.16	0.0E+00	BE007635.1	EST_HUMAN	QVQ-BN0147-280-400-213-g11 BN0147 Homo sapiens cDNA
4888	9878	15124	10.15	0.0E+00	4758189	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4887	9879	15126	1.35	0.0E+00	Y16723.1	NT	Homo sapiens gene encoding filensin, exon 8
4888	9880	15126	1.63	0.0E+00	6174560	NT	Homo sapiens meningioma expressed antigen 6 (colled-ocil proline-rich) (MGEA6), mRNA
4888	9880	15127	1.63	0.0E+00	6174560	NT	Homo sapiens meningioma expressed antigen 8 (colled-ocil proline-rich) (MGEA8), mRNA
4889	9881	15128	1.42	0.0E+00	7705546	NT	Homo sapiens zinc-finger DNA-binding protein (HJMHXY1), mRNA
4870	9882	15131	3.34	0.0E+00	AJ010442.1	NT	Homo sapiens mRNA for immunoglobulin kappa light chain, anti-RND, thereof 7
4873	9884	15131	6.4	0.0E+00	AF050588.1	NT	Homo sapiens MHC class 1 region
4875	9886	15134	2.08	0.0E+00	4505608	NT	Homo sapiens oploid receptor, delta 1 (OPRD1) mRNA
4876	9887	15134	2.43	0.0E+00	AF091711.1	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds
4880	9891	15138	1.15	0.0E+00	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
4880	10001	15147	0.88	0.0E+00	D83562.1	NT	Homo sapiens COL4A6 gene for $\alpha 6(V)$ collagen, exon 44 and partial cds
4894	10005	15149	1.58	0.0E+00	4503684	NT	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FDP5) mRNA
4894	10005	15149	1.58	0.0E+00	4503684	NT	Homo sapiens diacyltransferase 8 (alpha-N-acetylneuraminatase, alpha-2,8-diacyltransferase, GD3 synthase) (SIAT8) mRNA
4892	9818	14759	0.97	0.0E+00	4506982	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4914	10024	15168	1.18	0.0E+00	AB028898.1	NT	Homo sapiens chromosome 21 segment HS21C084
4932	10042	15182	1.47	0.0E+00	AL163284.2	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
4938	10048	15186	0.81	0.0E+00	7682319	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
4946	10055	15183	0.7	0.0E+00	AA205437.1	EST_HUMAN	z68606.c1 Strabagena neuroepithelium (8837231) Homo sapiens cDNA clone IMAGE:646547 3'
4950	10059	15187	1.45	0.0E+00	8922928	NT	Homo sapiens hypothetical protein FLJ11180 (FLJ11180), mRNA
4951	9898	15144	0.83	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4953	10061	15200	5.03	0.0E+00	4502368	NT	Homo sapiens beaded filament structural protein 1, fibronin (BFSP1) mRNA
4957	10066	15200	0.97	0.0E+00	U14967.1	NT	Human ribosomal protein L21 mRNA, complete cds
4987	10075	15213	1.88	0.0E+00	M10878.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
4989	10077	15218	2.72	0.0E+00	BE408863.1	EST_HUMAN	601303729F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3688118 5'
4978	10081	15218	6.21	0.0E+00	4758189	NT	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4981	10089	15222	1.12	0.0E+00	AB028968.1	NT	Homo sapiens mRNA for KIAA1043 protein, partial cds
4995	10101	15231	2.04	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
4995	10101	15232	2.04	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5007	10111	15240	0.78	0.0E+00	AA601246.1	EST_HUMAN	no14909.s1 NC1_CGAP_Fhet Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR-E239140 E239140 SPALT PROTEIN;

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Table 4
Single Exon Probes Expressed in BT474 Cells

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5007	10111	15241	0.78	0.0E+00	AA601246.1	EST_HUMAN	nc14g09.s1 NCI CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704.3' similar to TR:E239140
5007	10111	15242	0.78	0.0E+00	AA601246.1	EST_HUMAN	E239140 SPALT PROTEIN:
5013	5403	10347	0.87	0.0E+00	AF195658.1	NT	nc14g09.s1 NCI CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704.3' similar to TR:E239140
5018	10120	10347	0.84	0.0E+00	4758228	NT	E239140 SPALT PROTEIN:
5028	10130	15259	1.39	0.0E+00	AF016705.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
5036	10138		1.18	0.0E+00	AL163209.2	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5039	10141	18306	44.4	0.0E+00	D50657.1	NT	Homo sapiens EB-AIP ubiquitin-protein ligase (UBE3A) gene, exon 3
5069	10171	15307	3.62	0.0E+00	X52638.1	NT	Homo sapiens chromosome 21 segment H521C009
5070	10172	15307	0.72	0.0E+00	X72791.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
5102	10203	16342	1.17	0.0E+00	4657362	NT	Bacillus amyloquelidens sacB gene for levansucrase (EC 2.4.1.10)
5104	10205	16343	0.76	0.0E+00	5802055	NT	Human endogenous retrovirus mRNA for gag protein
5108	10209	16346	1.05	0.0E+00	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
5120	10221	16355	0.62	0.0E+00	6902091	NT	Homo sapiens SH2-containing protein Nap2 mRNA, complete cds
5121	10222	16356	1.03	0.0E+00	AF124250.1	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
5138	10238	16372	1.31	0.0E+00	7632421	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
5142	10242	16378	0.95	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
5142	10242	16378	0.96	0.0E+00	AF108830.1	NT	Human zinc finger protein zfp47 (zfp47) mRNA, partial cds
5143	10243	16380	0.91	0.0E+00	U71601.1	NT	Human sapiens chromosome 8 open reading frame 1 (ORF1) mRNA
5149	10249	16384	1.01	0.0E+00	4757889	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
5147	10247	16386	0.98	0.0E+00	AF195658.1	NT	Homo sapiens jumonji (mouse) homolog (JMJ) mRNA
5151	10251	16390	0.95	0.0E+00	4826777	NT	Homo sapiens mRNA for KIAA1613 protein, partial cds
5160	10260		0.94	0.0E+00	AB040946.1	NT	Homo sapiens mRNA for KIAA1613 protein, partial cds
5176	10276	16414	1.32	0.0E+00	BE144725.1	EST_HUMAN	CMO-HT0178-051089-084-e05 HT0178 Homo sapiens cDNA

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
5 from human Breast comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 5,205 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 5,206 - 10,317.
5. A spatially-addressable set of single exon nucleic acid
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Breast comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 5,205 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human Breast.

35

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 5,206 - 10,317 or a complementary sequence or a fragment thereof.

5

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Breast which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of
10 SEQ ID NOS.: 10,318 - 15,438, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human Breast.

16. A single exon nucleic acid probe as claimed in any one
15 of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

17. A single exon nucleic acid probe as claimed in any one
20 of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

25

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

30 20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

21. A single exon nucleic acid probe as claimed in any one
35 of claims 13 - 20, wherein said probe lacks homopolymeric

stretches of A or T.

22. A method of measuring gene expression in a sample derived from human Breast, comprising:

5 contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human Breast; and then measuring the label detectably bound to each probe of
10 said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

15 algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe, wherein said detectably labeled nucleic acids are derived from mRNA from the Breast of said eukaryote, said probe is
20 a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a microarray according to claim 12, and said fragment is selectively hybridizable at high stringency.

25 24. A method of assigning exons to a single gene, comprising:

30 identifying a plurality of exons from genomic sequence according to the method of claim 23; and then measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,
35 wherein a common pattern of expression of said exons in

said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

25. A nucleic acid sequence as set out in any of SEQ ID
5 NOS: 1 - 10,317 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of
SEQ ID Nos: 1 - 10,317.

10 27. A peptide comprising a sequence as set out in any of
SEQ ID Nos: 10,318 - 15,438.

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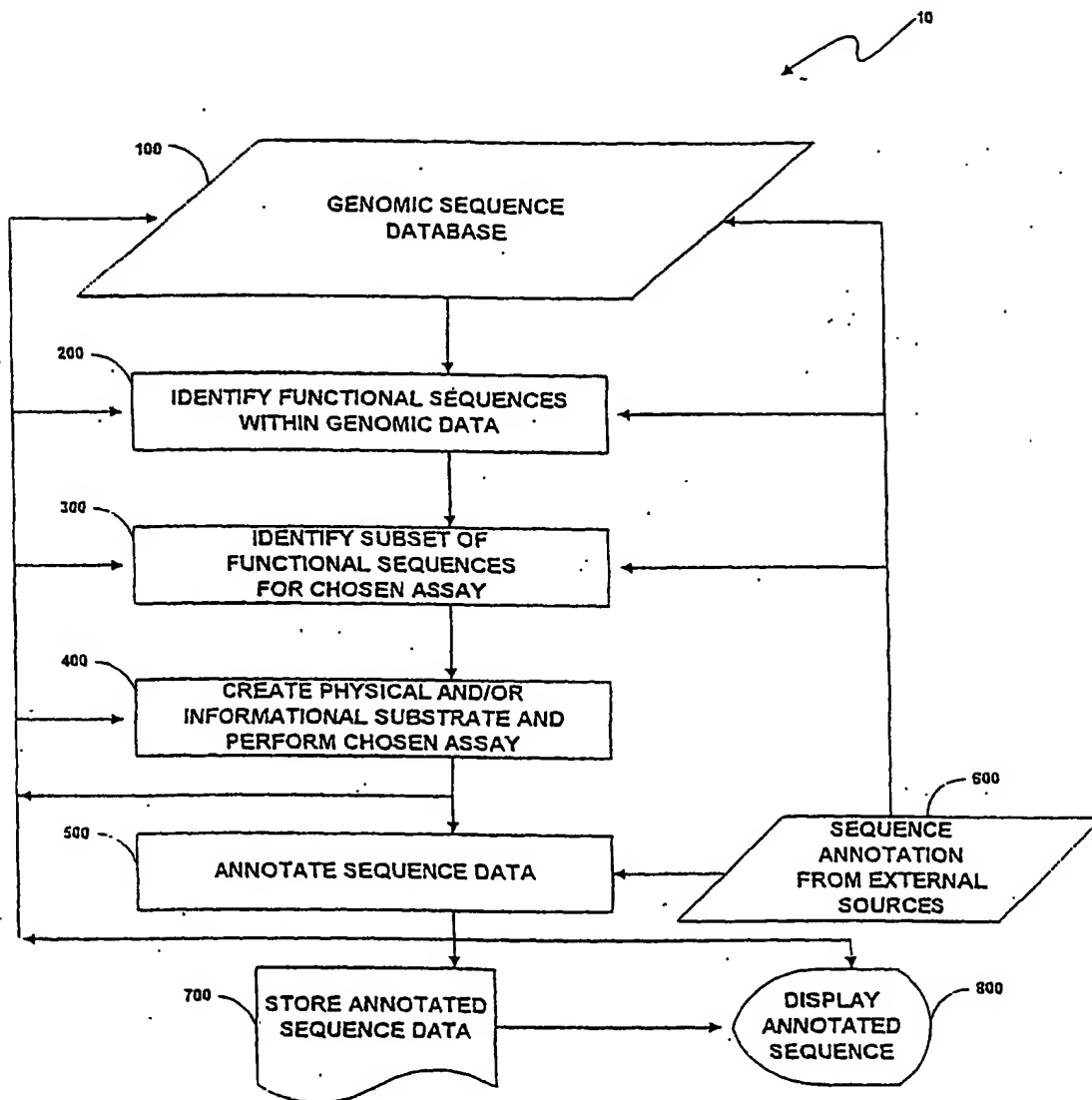


Fig. 1

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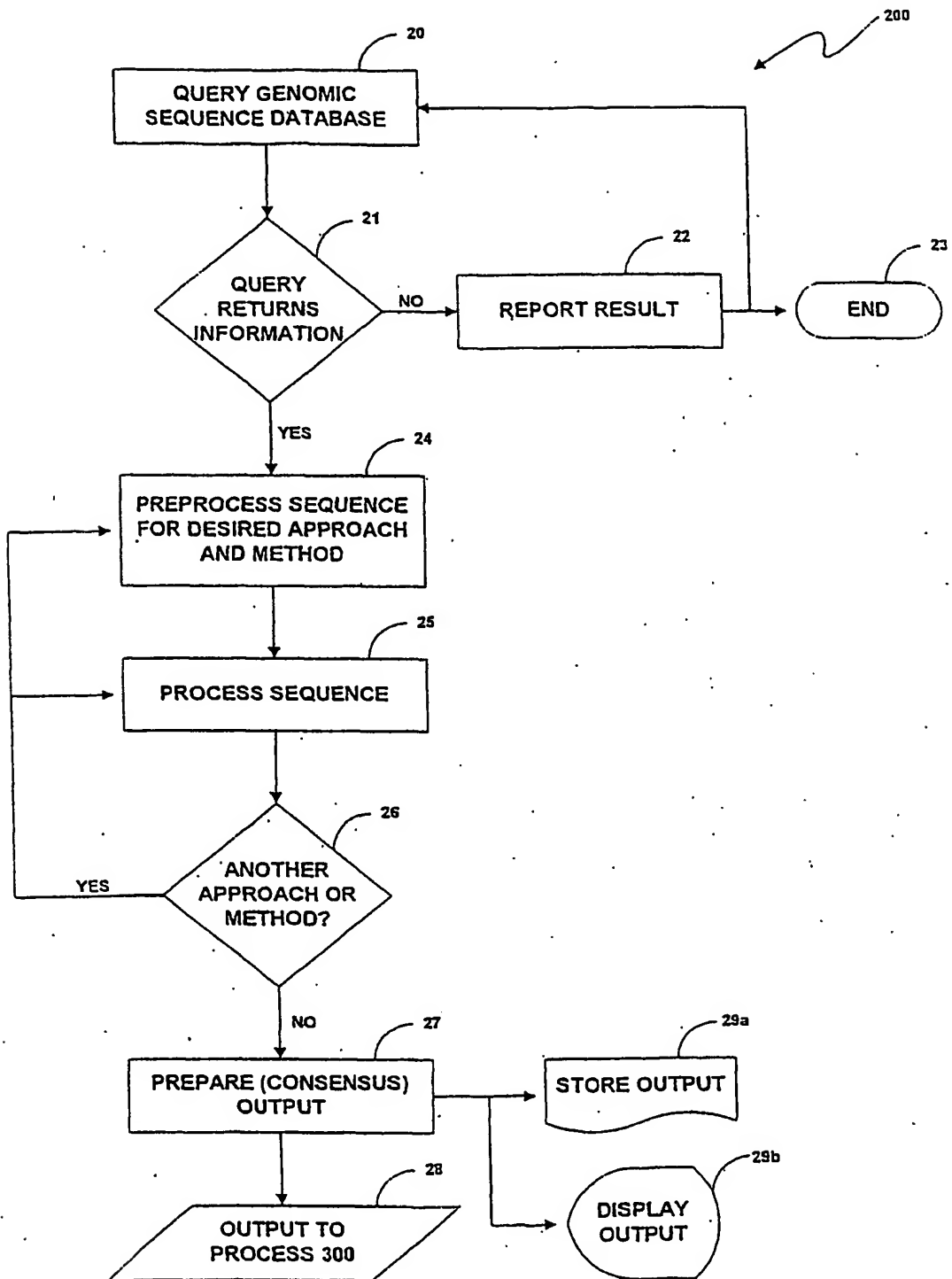


Fig. 2

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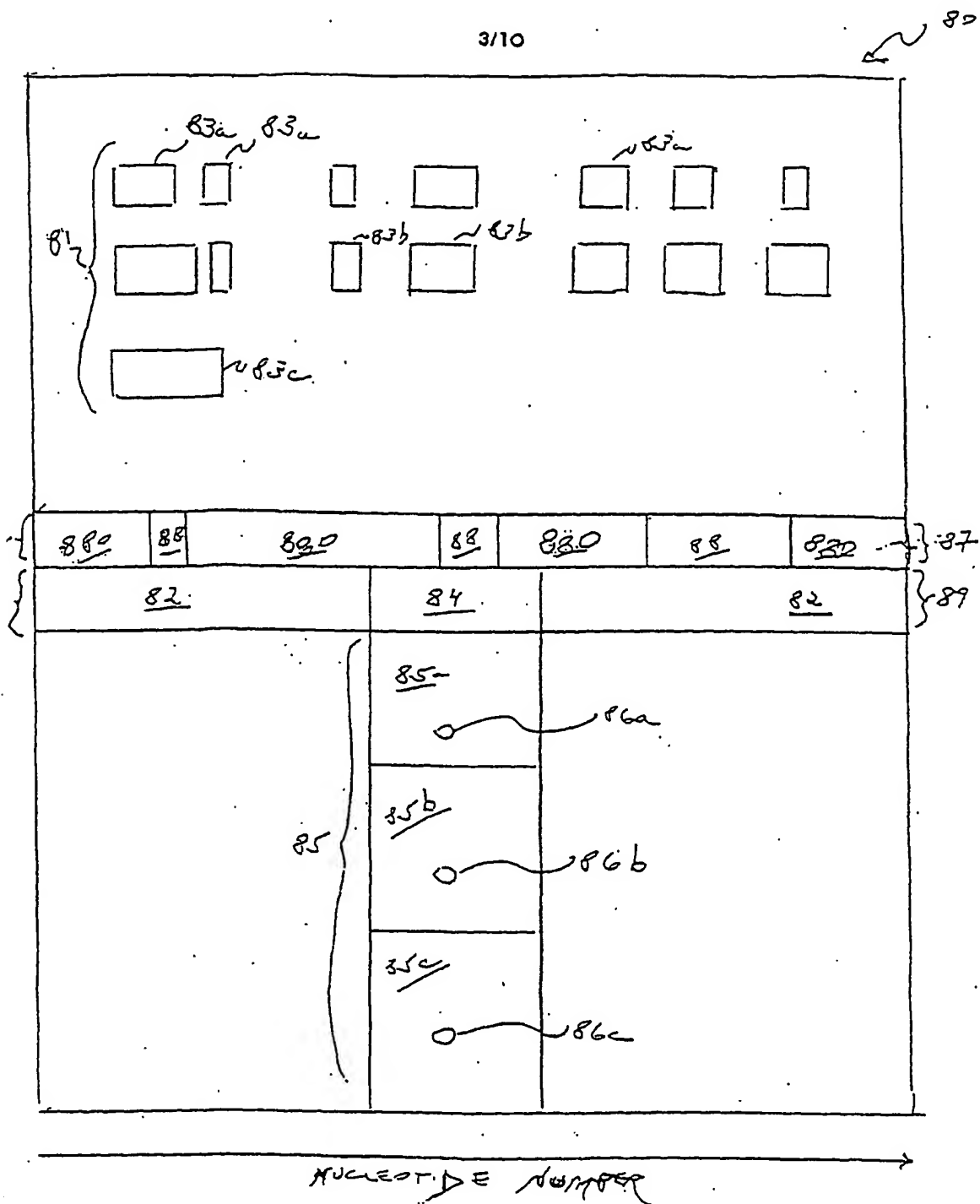


Fig. 3

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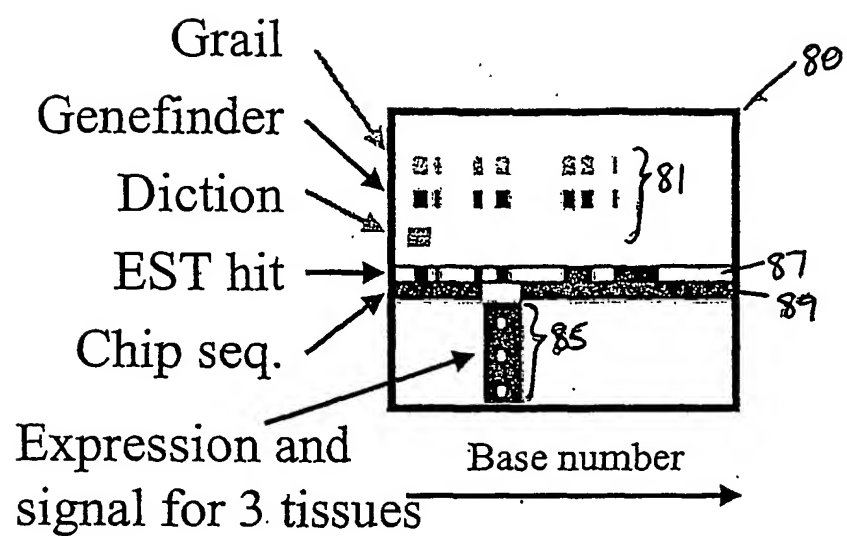


Fig. 4

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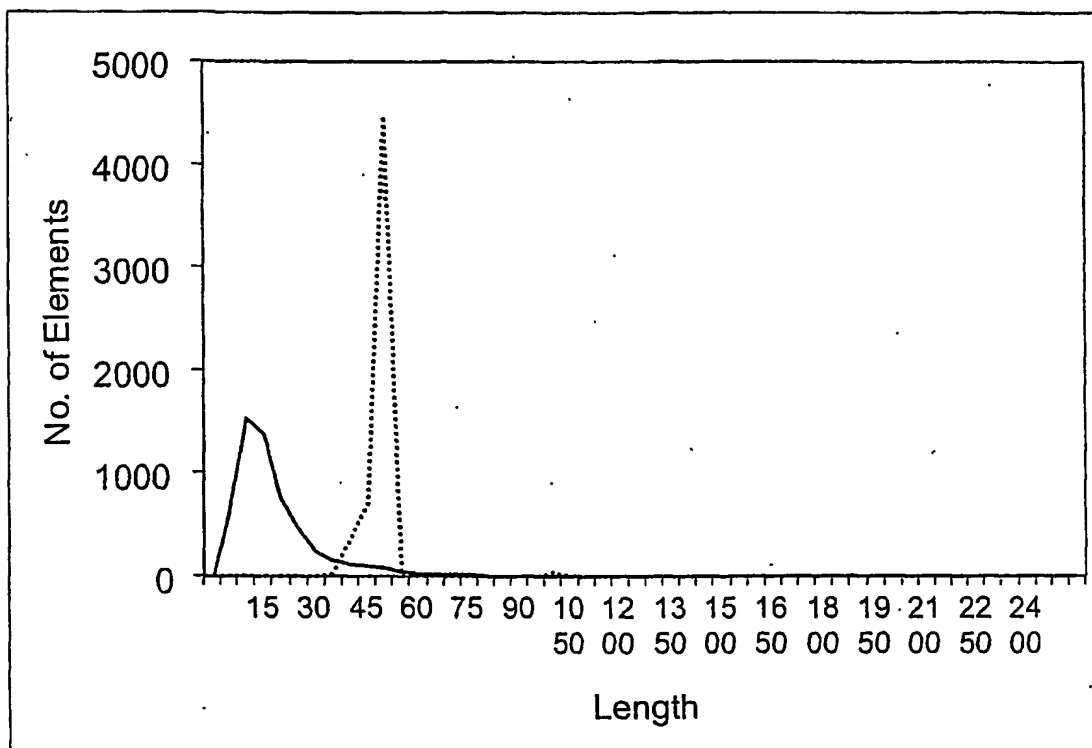


Fig. 5

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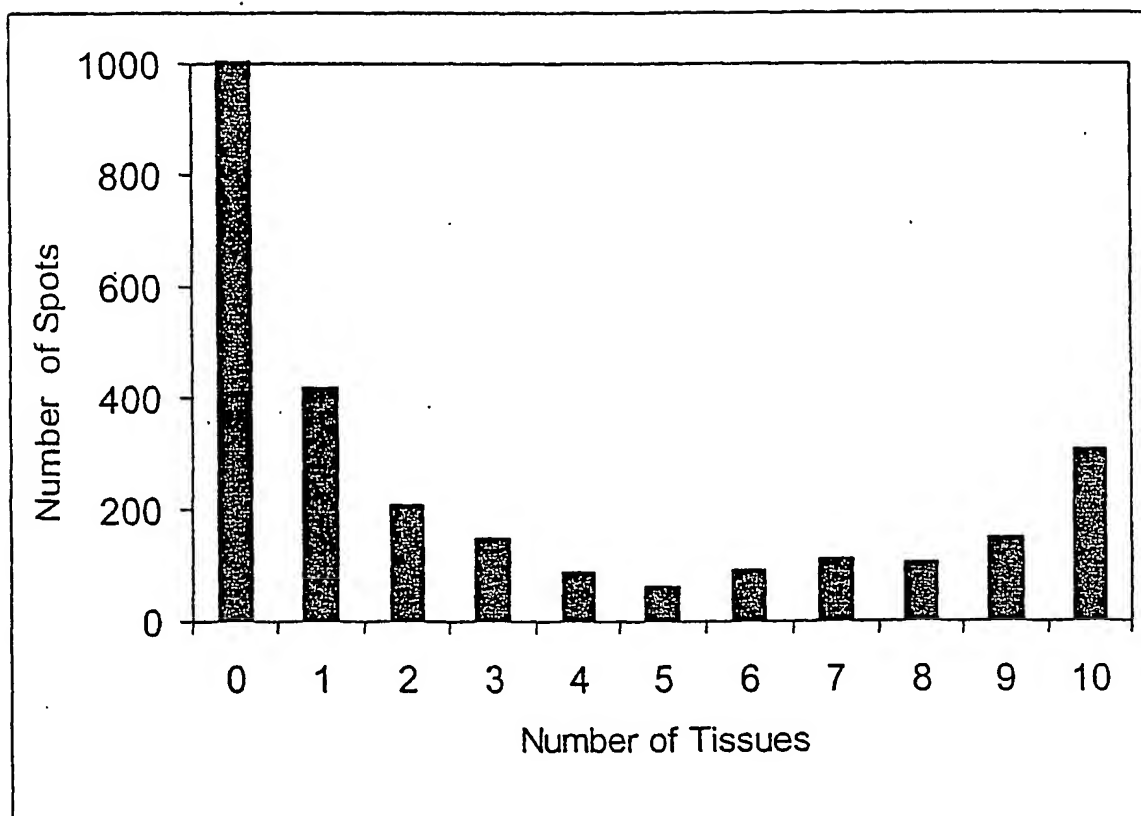


Fig. 6

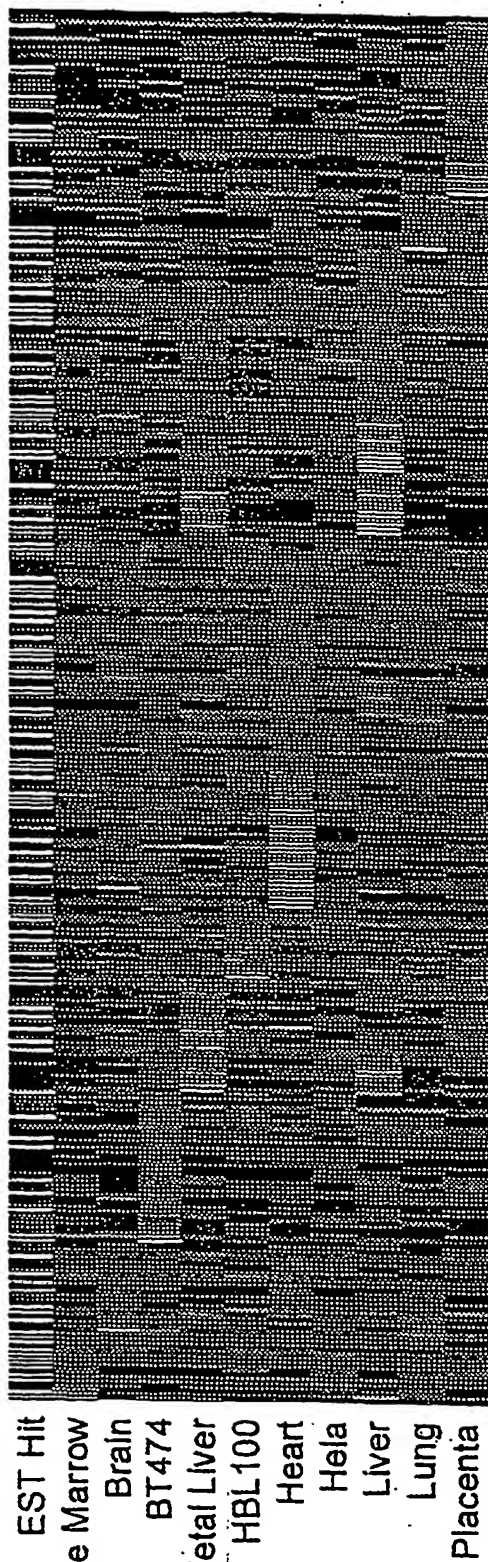


Fig. 7a

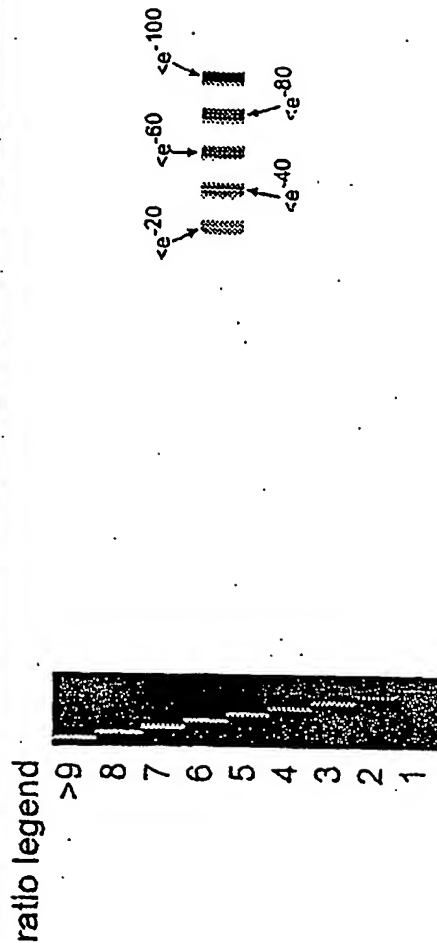


Fig. 7b

Fig. 7c

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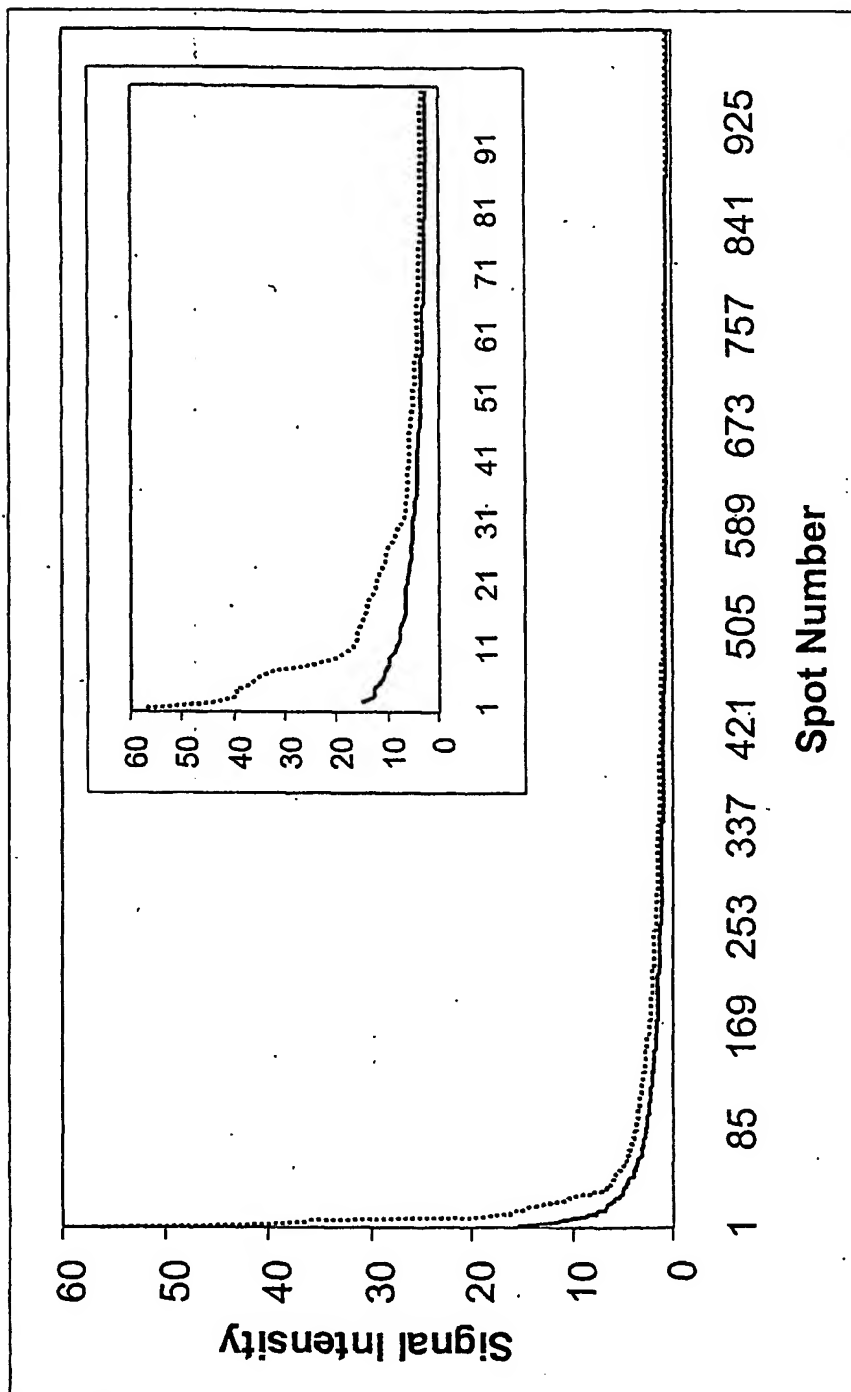


Fig. 8

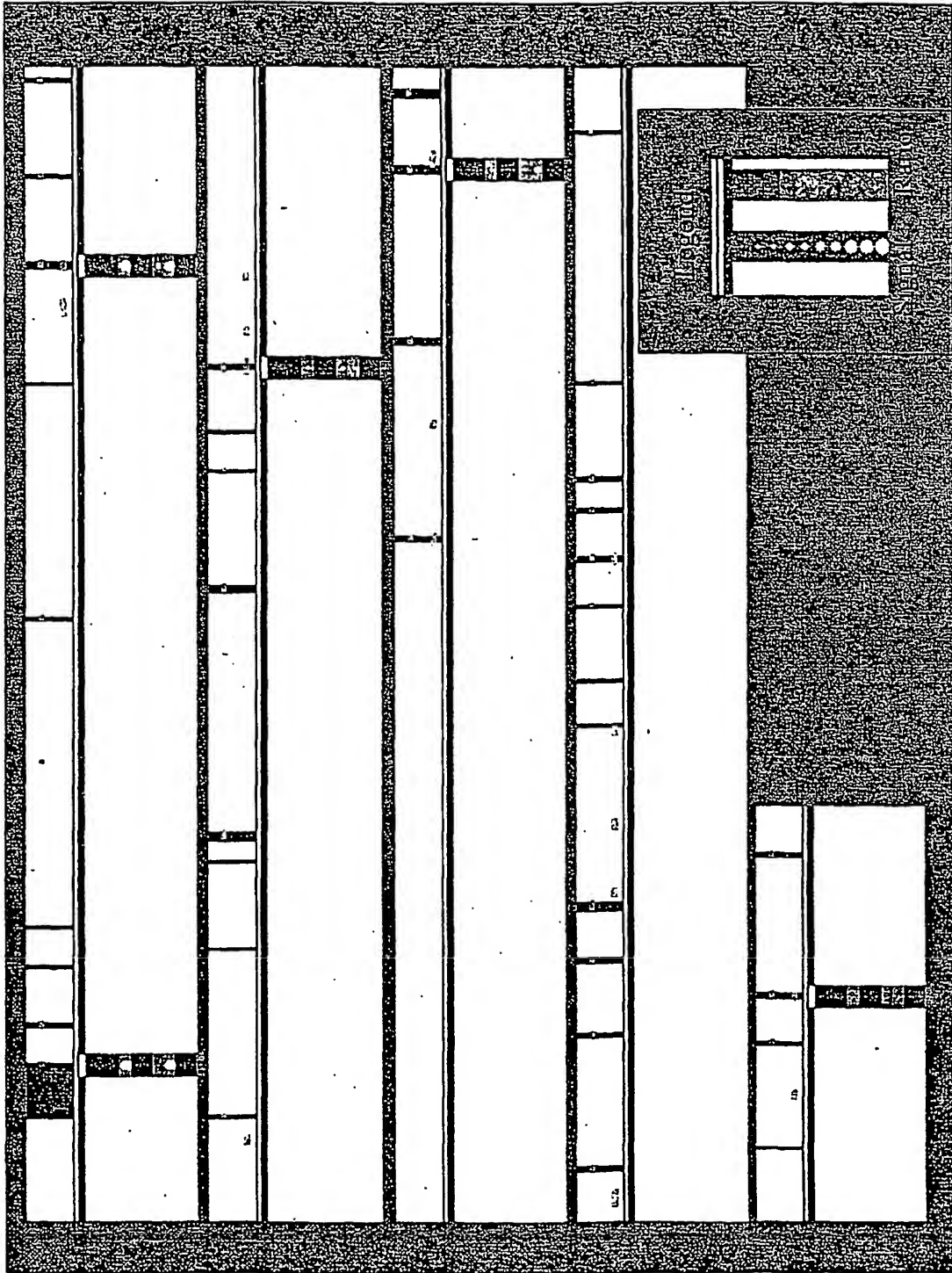
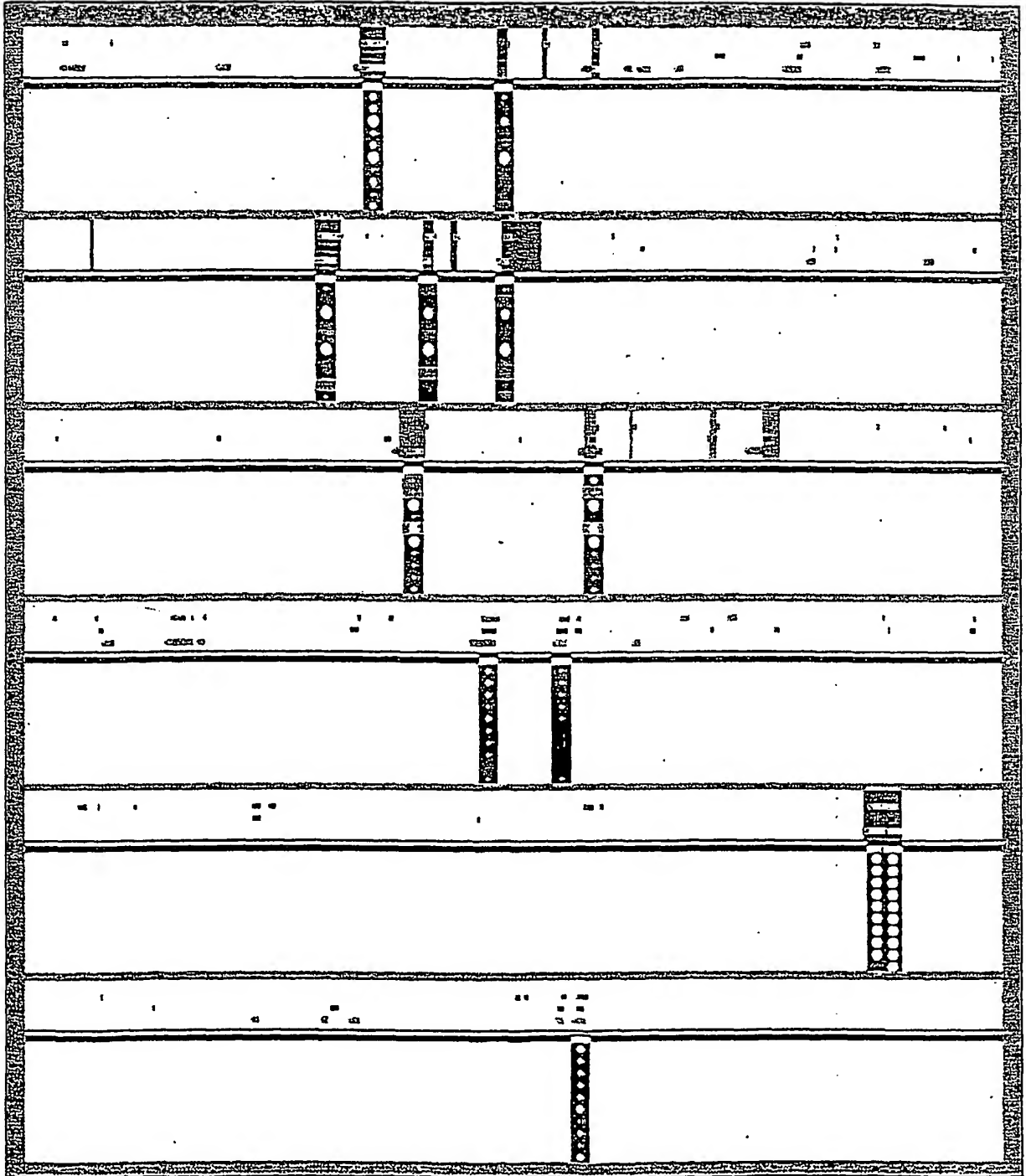


Fig. 9

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Fig. 10



(19) World Intellectual Property Organization
International Bureau



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9 August 2001 (09.08.2001)

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Published:

- with international search report
- with sequence listing part of description published separately in electronic form and available upon request from the International Bureau

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(74) Agent: **RONNING, Royal, N., Jr.**; Amersham Pharmacia Biotech, Inc., 800 Centennial Avenue, Piscataway, NJ 08855 (US).

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN BREAST AND BT 474 CELLS

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human BT 474 cells is described. Also described are single exon nucleic acid probes expressed in the BT 474 cells and their use in methods for detecting gene expression.

WO 01/057271 A3

INTERNATIONAL SEARCH REPORT

 International Application No
 PCT/US 01/00662

 A. CLASSIFICATION OF SUBJECT MATTER
 IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

 Minimum documentation searched (classification system followed by classification symbols)
 IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, BIOSIS, CHEM ABS Data, EMBASE, SCISEARCH, MEDLINE, EMBL

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL 'Online! 11 May 1999 (1999-05-11) HEILIG ET AL.: "Sequencing of the human chromosome 14" Database accession no. AL049837 XP002182997	13-21, 25
Y	abstract	1-12, 22-24, 26, 27

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents:

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
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Date of the actual completion of the international search

12 July 2002

Date of mailing of the international search report

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Bort, S

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/00662

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL 'Online! 14 November 1997 (1997-11-14) ADAMS ET AL.: "Use of a random BAC End sequence database for sequence-ready map building" Database accession no. B57793 XP002186124</p>	13-21,25
Y	<p>abstract</p>	1-12, 22-24, 26,27
X	<p>DATABASE EMBL 'Online! 9 May 1997 (1997-05-09) MARRA ET AL.: "The WashU-HHMI Mouse EST Project" Database accession no. AA414703 XP002205620</p>	13-21,25
Y	<p>abstract</p>	1-12, 22-24, 26,27
X	<p>DATABASE SWALL 'Online! 1 July 1997 (1997-07-01) "pro-pol-dutpase polyprotein (fragment)" Database accession no. 002711 XP002037954 abstract & BENIT ET AL.: "Cloning of a new murine endogenous retrovirus, MuERV-L, with strong similarity to the human HERV-L element with a gag coding sequence closely related to the Fv1 restriction gene" J. VIROL., vol. 71, 1997, page 5652</p>	26,27
Y	<p>W0 98 30722 A (MACK DAVID H) 16 July 1998 (1998-07-16) the whole document</p>	1-12, 22-24
Y	<p>BURGE C ET AL: "Prediction of complete gene structure in human genomic DNA" JOURNAL OF MOLECULAR BIOLOGY, LONDON, GB, vol. 268, no. 1, 25 April 1997 (1997-04-25), pages 78-94, XP002109301 ISSN: 0022-2836 the whole document</p>	1-12, 22-24, 26,27
Y	<p>CHURCH D M ET AL: "ISOLATION OF GENES FROM COMPLEX SOURCES OF MAMMALIAN GENOMIC DNA USING EXON AMPLIFICATION" NATURE GENETICS, NEW YORK, NY, US, vol. 6, 1994, pages 98-105, XP000608940 ISSN: 1061-4036 the whole document</p>	1-12, 22-24, 26,27
	-/-	

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 01/00662

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	LIPSHUTZ R J ET AL: "High density synthetic oligonucleotide arrays." NATURE GENETICS, (1999 JAN) 21 (1 SUPPL) 20-4. REF: 32 , XP002182912 the whole document _____	1-12

INTERNATIONAL SEARCH REPORT

national application No.
PCT/US 01/00662

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this International application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee; this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
1-27 (all partially)
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

The following statements about the impossibility of performing a meaningful search according to Art. 17(2) PCT are made for the subject matter for which a search has been performed and identified as the first and second inventions in form 206 PCT.

Present claims 1-12 and 22-24 relate to an extremely large number of possible sets of nucleic acid probes comprising Seq. Id 1 or 2, as well as microarrays comprising said sets. In fact, the claims contain so many possible permutations, that a lack of conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search over the whole of the claimed scope impossible. Consequently, the search for the sets of probes comprising Seq. Id 1 or 2 has been limited to the Seq. Id as such.

Claims 1-3, 5, 6, 8-15 and 18-24 relate to portions or fragments of nucleic acids defined by Seq. Id. 1 or 2. The length or other similar characterizing features of the portions or fragments is not disclosed, bringing the total number of possible prior art sequences to exceptionally high numbers. The shorter the length, the higher the possibility that an overflow of, in principle unrelated, sequences are retrieved, making the establishment of a meaningful International Search Report impossible. For this reason the search has been limited to portions or fragments of Seq. Id. 1 or 2 having a significant minimum length and being supported by the description, namely at least 15 contiguous nucleotides (see claim 16).

Claims 15-21 relate to an extremely large number of nucleic acid probes. The probes are defined solely by their potential to code for peptide Seq. Id. 10326. However, due to the degeneracy of the genetic code, every peptide is potentially coded by an extremely high number of nucleic acid sequences. In fact, the claims contain so many potential nucleic acid sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search over the whole of the claimed scope impossible. The search has therefore been carried out for those parts of the claim which do appear to be clear and concise, namely the nucleic acid sequences disclosed in the application and identified as encoding the referred peptide in table 4 (Seq. Ids. 1 or 2 and 5214).

Likewise, claim 26, which refers to peptides encoded by Seq. Id. 1 or 2 and 5214, encompasses a high and undefined number of possible peptides. Besides three possible reading frames deriving from the encoding nucleic acid strand, as well as three additional reading frames deriving from the complementary nucleic acid strand, every possible fragment of these is being covered by the claim. This is due to the potential presence of stop codons within any of the six possible reading frames which can not be established a priori. Thus, claim 26 contains so many potential peptide sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search over the whole of the claimed scope impossible. Consequently, the search has been carried out for those parts of the claim which do appear to be

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

clear and concise, namely the peptide disclosed, identified by Seq. Id. 10326.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-27 (all partially)

A nucleic acid probe comprising SEQ ID 1, complementary sequences or fragments thereof (in particular comprising SEQ ID 5214). Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptide encoded by SEQ ID 1 (in particular the one defined by SEQ ID 10326).

Invention 2: claims 1-27 (all partially)

A nucleic acid probe comprising SEQ ID 2, complementary sequences or fragments thereof (in particular comprising SEQ ID 5214). Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptide encoded by SEQ ID 2 (in particular the one defined by SEQ ID 10326).

Inventions 3-5205: claims 1-27 (all partially)

A nucleic acid probe comprising SEQ ID n (where n ranges from 3-5205 according to the invention number above), complementary sequences or fragments thereof, in particular comprising the SEQ ID no. which is listed in the column "Exon SEQ ID no." in the same row that contains SEQ ID n in table 4. Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptide encoded by SEQ ID n, in particular the one defined by the SEQ ID no in the column "ORF SEQ ID no" of the same row where SEQ ID n is listed.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 01/00662

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9830722 A	16-07-1998	AU 6035698 A	03-08-1998
		EP 0973939 A1	26-01-2000
		JP 2001508303 T	26-06-2001
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